GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 5, 2004, 16:40:19 ; Search time 6893 Seconds
(without alignments)
11343.513 Million cell updates/sec

Title: US-09-668-314C-1
Perfect score: 1804
Sequence: 1 atgggcgcactggcccgggc.....aaaccaaaaaaaaaaaaaaa 1804

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
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11: gb_sts:*
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39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1804	100.0	1804	6	BD235885	BD235885 Alzheimer
2	1804	100.0	1804	6	AR224092	AR224092 Sequence
3	1804	100.0	1804	6	AR269223	AR269223 Sequence
4	1804	100.0	1804	6	AX105383	AX105383 Sequence
5	1804	100.0	1804	6	AX573821	AX573821 Sequence
6	1804	100.0	1804	9	AF200342	AF200342 Homo sapi
7	1790.6	99.3	2990	9	AF178532	AF178532 Homo sapi
8	1788.2	99.1	1885	9	AF200192	AF200192 Homo sapi
9	1784.4	98.9	1879	6	AX376004	AX376004 Sequence
10	1784.4	98.9	1879	9	AY358927	AY358927 Homo sapi
11	1768.2	98.0	1864	9	BC014453	BC014453 Homo sapi
12	1768.2	98.0	1873	6	BD231786	BD231786 Metastati
13	1768.2	98.0	1873	6	AR411231	AR411231 Sequence
14	1768.2	98.0	1873	9	AF117892	AF117892 Homo sapi
15	1765.6	97.9	1862	6	AR136909	AR136909 Sequence
16	1765.6	97.9	1862	6	E30679	E30679 ASP1. 6/200
17	1765.6	97.9	1862	6	AX775211	AX775211 Sequence
18	1765.6	97.9	1862	6	BD165905	BD165905 ASP1. 1/2
19	1765.6	97.9	1862	9	AF204944	AF204944 Homo sapi
20	1753.4	97.2	1863	6	AX351516	AX351516 Sequence
21	1753.4	97.2	1863	9	AF050171	AF050171 Homo sapi
22	1550	85.9	1621	9	AF212252	AF212252 Homo sapi
23	1483.6	82.2	1712	6	AX136403	AX136403 Sequence
24	1483.6	82.2	1712	6	BD123654	BD123654 Secretory
25	1483.6	82.2	1712	9	AK075539	AK075539 Homo sapi
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27	1478.6	82.0	2429	6	BD231769	BD231769 Metastati
28	1478.6	82.0	2429	6	AR411214	AR411214 Sequence
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33	1179.4	65.4	1774	10	AF216310	AF216310 Mus muscu

	34	1134.2	62.9	1545	6	AR170159	AR170159 Sequence
	35	1134.2	62.9	1545	6	AR201145	AR201145 Sequence
	36	1104.6	61.2	2514	6	AR263854	AR263854 Sequence
	37	953.6	52.9	1021	6	AR263907	AR263907 Sequence
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c	43	496	27.5	554	6	AX136731	AX136731 Sequence
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ALIGNMENTS

RESULT 1
BD235885
LOCUS BD235885 1804 bp DNA linear PAT 17-JUL-2003
DEFINITION Alzheimer's disease secretase.
ACCESSION BD235885
VERSION BD235885.1 GI:33045655
KEYWORDS JP 2002526081-A/1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1804)
AUTHORS Gurney,M.E., Bienkowski,M.J., Heinrikson,R.L., Parodi,L.A. and
Yan,R.
TITLE Alzheimer's disease secretase
JOURNAL Patent: JP 2002526081-A 1 20-AUG-2002;
PHARMACIA AND UPJOHN CO
COMMENT OS Homo sapiens (human)
PN JP 2002526081-A/1
PD 20-AUG-2002
PF 23-SEP-1999 JP 2000574268
PR 24-SEP-1998 US 60/101594
PI MARK E GURNEY,MICHAEL JEROME BIENKOWSKI,ROBERT LEROY PI
HEINRIKSON,
PI LUIS A PARODI,RIQIANG YAN
PC C12N15/09,A61K45/00,A61P25/28,C07K14/47,C07K16/18,C12N1/15, PC
C12N1/19,
PC
C12N1/21,C12N5/10,C12N9/64,C12P21/02,C12P21/08,C12Q1/37,G01N33/ PC
15,
PC G01N33/50//(C12N1/21,C12R1:19),C12N15/00,C12N5/00 CC
Alzheimer's disease secretase
FH Key Location/Qualifiers
FT source 1. .1804
FT /organism='Homo sapiens (human)'.
FEATURES Location/Qualifiers
source 1. .1804
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 1804; DB 6; Length 1804;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1804; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60
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Db          1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60

Qy         61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120
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Qy        121 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180
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Qy        181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240
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Qy       1081 TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1140
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DEFINITION  Sequence 1 from patent US 6440698.
ACCESSION   AR224092
VERSION     AR224092.1  GI:23332752
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1804)
  AUTHORS   Gurney,M.E., Bienkowski,M.J., Heinrikson,R.L., Parodi,L.A. and
            Yan,R.
  TITLE     Alzheimer's disease secretase, APP substrates therefor, and uses
            therefor
  JOURNAL   Patent: US 6440698-A 1 27-AUG-2002;
FEATURES             Location/Qualifiers
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ORIGIN

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  Matches 1804;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy        421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480
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Db        421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480

Qy        481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540
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Qy        541 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600
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Qy       1081 TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1140
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Db       1141 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA 1200

Qy       1201 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC 1260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC 1260

Qy       1261 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1320
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Db       1261 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1320

Qy       1321 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1380
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Db       1321 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1380

Qy       1381 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1440
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Db       1381 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1440

Qy       1441 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1500
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Db       1441 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1500

Qy       1501 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1560
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Db       1501 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1560

Qy       1561 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1620
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Db       1561 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1620

Qy       1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1680
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Db       1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1680

Qy       1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740

Qy       1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAAACCAAAAAAAAAAA 1800
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Db       1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAAACCAAAAAAAAAAA 1800

Qy       1801 AAAA 1804
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Db       1801 AAAA 1804
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RESULT 3
AR269223
LOCUS AR269223 1804 bp DNA linear PAT 10-APR-2003

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DEFINITION  Sequence 1 from patent US 6500667.
ACCESSION   AR269223
VERSION     AR269223.1  GI:29700191
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1804)
  AUTHORS   Gurney,M.E., Bienkowski,M.J., Heinrikson,R.L., Parodi,L.A. and
            Yan,R.
  TITLE     Aspartyl protease 2 (Asp2) antisense oligonucleotides
  JOURNAL   Patent: US 6500667-A 1 31-DEC-2002;
FEATURES             Location/Qualifiers
     source          1. .1804
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                     /mol_type="genomic DNA"
ORIGIN

  Query Match             100.0%;  Score 1804;  DB 6;  Length 1804;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1804;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy         61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120

Qy        121 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180

Qy        181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240
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Db        181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240

Qy        241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300
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Db        241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300

Qy        301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360
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Db        301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360

Qy        361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420
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Db        361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420

Qy        421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480
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Db        421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480

Qy        481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540
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Db        481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540
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Qy        541 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600
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Db        541 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600

Qy        601 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 660
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Db        601 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 660

Qy        661 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 720
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Db        661 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 720

Qy        721 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 780
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Db        721 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 780

Qy        781 GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA 840
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Db        781 GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA 840

Qy        841 TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC 900
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Db        841 TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC 900

Qy        901 ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG 960
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Qy        961 GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC 1020

Qy       1021 CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC 1080

Qy       1081 TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1140
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Db       1081 TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1140

Qy       1141 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA 1200

Qy       1201 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC 1260

Qy       1261 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1320

Qy       1321 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1380
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Qy       1381 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1440
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Db       1381 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1440

Qy       1441 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1500
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Qy       1501 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1560
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Qy       1561 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1620
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Qy       1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1680

Qy       1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740

Qy       1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAAACCAAAAAAAAAAA 1800
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAAACCAAAAAAAAAAA 1800

Qy       1801 AAAA 1804
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Db       1801 AAAA 1804
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AX105383
LOCUS       AX105383                1804 bp    DNA     linear   PAT 30-APR-2001
DEFINITION  Sequence 1 from Patent WO0123533.
ACCESSION   AX105383
VERSION     AX105383.1  GI:13921510
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Gurney,M. and Bienkowski,M.J.
  TITLE     Alzheimer's disease secretase, app substrates therefor, and uses
            therefor
  JOURNAL   Patent: WO 0123533-A 1 05-APR-2001;
            Pharmacia & Upjohn Company (US)
FEATURES             Location/Qualifiers
     source          1. .1804
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
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Query Match 100.0%; Score 1804; DB 6; Length 1804;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1804; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60
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Db          1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60

Qy         61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120

Qy        121 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180
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Db        121 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180

Qy        181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240
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Db        181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240

Qy        241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300

Qy        301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360
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Db        301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360

Qy        361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420

Qy        421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480

Qy        481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540
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Db        481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540

Qy        541 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600
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Db        541 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600

Qy        601 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 660
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Db        601 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 660

Qy        661 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 720
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Db        661 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 720

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Db        721 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 780

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Db        781 GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA 840

Qy        841 TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC 900
Db        841 TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC 900

Qy        901 ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG 960
Db        901 ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG 960

Qy        961 GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC 1020
Db        961 GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC 1020

Qy       1021 CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC 1080
Db       1021 CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC 1080

Qy       1081 TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1140
Db       1081 TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1140

Qy       1141 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA 1200
Db       1141 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA 1200

Qy       1201 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC 1260
Db       1201 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC 1260

Qy       1261 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1320
Db       1261 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1320

Qy       1321 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1380
Db       1321 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1380

Qy       1381 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1440
Db       1381 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1440

Qy       1441 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1500
Db       1441 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1500

Qy       1501 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1560
Db       1501 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1560

Qy       1561 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1620
Db       1561 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1620

Qy       1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1680
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Db        1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1680

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Qy        1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAAACCAAAAAAAAAAA 1800
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Db        1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAAACCAAAAAAAAAAA 1800

Qy        1801 AAAA 1804
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Db        1801 AAAA 1804
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RESULT 5
AX573821
LOCUS       AX573821                1804 bp    DNA     linear   PAT 07-JAN-2003
DEFINITION  Sequence 1 from Patent EP1249498.
ACCESSION   AX573821
VERSION     AX573821.1  GI:27551476
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Gurney,M. and Bienkowski,M.J.
  TITLE     Alzheimer's disease secretase, app substrates therefor, and uses
            therefor
  JOURNAL   Patent: EP 1249498-A 1 16-OCT-2002;
            PHARMACIA & UPJOHN COMPANY (US)
FEATURES             Location/Qualifiers
     source          1. .1804
                     /organism="Homo sapiens"
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ORIGIN

  Query Match           100.0%;  Score 1804;  DB 6;  Length 1804;
  Best Local Similarity 100.0%;  Pred. No. 0;
  Matches 1804;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60
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Db          1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60

Qy         61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120
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Db         61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120

Qy        121 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180
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Qy        181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240
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Db        181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240

Qy        241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300
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Db        301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360

Qy        361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420
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Qy        421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480
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Db        421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480

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Db        541 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600

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Qy        841 TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC 900
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Qy        901 ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG 960
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Qy       1081 TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1140
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Qy       1801 AAAA 1804
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Db       1801 AAAA 1804
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RESULT 6
AF200342
LOCUS AF200342 1804 bp mRNA linear PRI 12-DEC-1999

DEFINITION Homo sapiens chromosome 21 aspartyl protease 1 mRNA, complete cds.
ACCESSION AF200342
VERSION AF200342.1 GI:6561811
KEYWORDS .
SOURCE Homo sapiens (human)
  ORGANISM Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1804)
  AUTHORS Yan,R., Bienkowski,M.J., Shuck,M.E., Miao,H., Tory,M.C.,
  Pauley,A.M., Brashier,J.R., Stratman,N.C., Mathews,W.R., Buhl,A.E.,
  Carter,D.B., Tomasselli,A.G., Parodi,L.A., Heinrikson,R.L. and
  Gurney,M.E.
  TITLE Membrane-anchored aspartyl protease with Alzheimer's disease
  beta-secretase activity
  JOURNAL Nature 402 (6761), 533-537 (1999)
  MEDLINE 20057170
   PUBMED 10591213
REFERENCE 2 (bases 1 to 1804)
  AUTHORS Bienkowski,M.J., Shuck,M.E., Slightom,J.L. and Drong,R.F.
  TITLE Direct Submission
  JOURNAL Submitted (29-OCT-1999) Genomics Research, Pharmacia&Upjohn, 301
  Henrietta, Kalamazoo, MI 49007, USA
FEATURES Location/Qualifiers
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  CYRFGISPSTNALVIGATVMEGFYVIFDRAQKRVGFAASPCAEIAGAAVSEISGPFST
  EDVASNCVPAQSLSEPILWIVSYALMSVCGAILLVLIVLLLLPFRCQRRPRDPEVVND
  ESSLVRHRWK"
ORIGIN

Query Match 100.0%; Score 1804; DB 9; Length 1804;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1804; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60
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Qy         61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120
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Qy        121 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180
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Qy        361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420
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Db        361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420

Qy        421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480
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Db        421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480

Qy        481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540
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Db        481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540

Qy        541 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600
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Db        541 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600

Qy        601 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 660
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Qy        901 ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG 960
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Db        901 ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG 960
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Qy        961 GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC 1020
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Qy       1021 CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC 1080
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Qy       1201 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC 1260
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Db       1201 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC 1260
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Qy       1261 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1320
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Qy       1801 AAAA 1804
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Db          1801 AAAA 1804


RESULT 7
AF178532
LOCUS       AF178532                2990 bp    mRNA    linear   PRI 21-SEP-2000
DEFINITION  Homo sapiens aspartyl protease (BACE2) mRNA, complete cds.
ACCESSION   AF178532
VERSION     AF178532.1  GI:6851265
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2990)
  AUTHORS   Solans,A., Estivill,X. and de La Luna,S.
  TITLE     A new aspartyl protease on 21q22.3, BACE2, is highly similar to
            Alzheimer's amyloid precursor protein beta-secretase
  JOURNAL   Cytogenet. Cell Genet. 89 (3-4), 177-184 (2000)
   MEDLINE  20422477
    PUBMED  10965118
REFERENCE   2  (bases 1 to 2990)
  AUTHORS   Solans,A., Estivill,X. and de la Luna,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-AUG-1999) Medical and Molecular Genetics Center, IRO,
            Avia. Castelldefels Km 2,7, L'Hospitalet de Llobregat, Barcelona
            08907, Spain
FEATURES             Location/Qualifiers
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/gene="BACE2"
ORIGIN

Query Match 99.3%; Score 1790.6; DB 9; Length 2990;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1793; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy          1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        464 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 523

Qy         61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120
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Db        524 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 583

Qy        121 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        584 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 643

Qy        181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        644 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 703

Qy        241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        704 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 763

Qy        301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360
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Db        764 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 823

Qy        361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420
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Db        824 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 883

Qy        421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480
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Db        884 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 943

Qy        481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540
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Db        944 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 1003

Qy        541 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600
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Db       1004 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 1063

Qy        601 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 660
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Qy        661 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 720
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Qy        721 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 780
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Db       1184 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 1243

Qy        781 GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA 840
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Db       1244 GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA 1303

Qy        841 TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC 900
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Db       1304 TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC 1363

Qy        901 ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG 960
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Db       1364 ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG 1423

Qy        961 GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC 1020
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Db       1424 GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC 1483

Qy       1021 CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC 1080
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Db       1484 CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC 1543

Qy       1081 TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1140
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Db       1544 TACCTGAGAGACGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1603

Qy       1141 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA 1200
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Db       1604 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA 1663

Qy       1201 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC 1260
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Qy       1261 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1320
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Qy       1321 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1380
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Qy       1381 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1440
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Db       1844 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1903

Qy       1441 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1500
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Db       1904 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1963

Qy       1501 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1560
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Db       1964 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 2023

Qy       1561 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2024 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 2083
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Qy       1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1680
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Db       2084 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 2143

Qy       1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740
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Db       2144 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 2203

Qy       1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAAACCAAAAAAAA 1797
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Db       2204 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAAACCAAAACAGA 2260
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RESULT 8
AF200192

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LOCUS       AF200192                1885 bp    mRNA    linear   PRI 16-FEB-2000
DEFINITION  Homo sapiens memapsin 1 mRNA, complete cds.
ACCESSION   AF200192
VERSION     AF200192.1  GI:6470290
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1885)
  AUTHORS   Lin,X., Koelsch,G., Wu,S., Downs,D., Dashti,A. and Tang,J.
  TITLE     Human aspartic protease memapsin 2 cleaves the beta-secretase site
            of beta-amyloid precursor protein
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (4), 1456-1460 (2000)
  MEDLINE   20144060
   PUBMED   10677483
REFERENCE   2  (bases 1 to 1885)
  AUTHORS   Lin,X., Koelsch,G. and Tang,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (28-OCT-1999) Protein Studies Program, Oklahoma Medical
            Research Foundation, 825 N.E. 13th Street, Oklahoma City, OK 73104,
            USA
FEATURES             Location/Qualifiers
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                     /codon_start=1
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                     DLVTIPKGFNTSFLVNIATIFESENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSL
                     VTQANIPNVFSMQMCGAGLPVAGSGTNGGSLVLGGIEPSLYKGDIWYTPIKEEWYYQI
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GFWTGSQLACWTNSETPWSYFPKISIYLRDENSSRSFRITILPQLYIQPMMGAGLNYE
CYRFGISPSTNALVIGATVMEGFYVIFDRAQKRVGFAASPCAEIAGAAVSEISGPFST
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ESSLVRHRWK"

ORIGIN

Query Match 99.1%; Score 1788.2; DB 9; Length 1885;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1801; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

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Qy          1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         78 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 137

Qy         61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120
              |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db        138 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGACCGCGGCCACGAAC 197

Qy        121 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        198 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 257

Qy        181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        258 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 317

Qy        241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        318 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 377

Qy        301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        378 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 437

Qy        361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        438 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 497

Qy        421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        498 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 557

Qy        481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        558 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 617

Qy        541 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600
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Db        618 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 677

Qy        601 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 660
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Db        678 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 737

Qy        661 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        738 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 797
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Qy        721 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        798 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 857

Qy        781 GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA 840
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Db        858 GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA 917

Qy        841 TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC 900
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Db        918 TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC 977

Qy        901 ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG 960
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Db        978 ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG 1037

Qy        961 GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC 1020
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Db       1038 GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC 1097

Qy        1021 CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC 1080
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Db        1098 CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC 1157

Qy        1081 TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1140
               |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        1158 TACCTGAGAGACGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1217

Qy        1141 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA 1200
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1218 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA 1277

Qy        1201 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC 1260
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Db        1278 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC 1337

Qy        1261 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1320
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Db        1338 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1397

Qy        1321 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1380
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Db        1398 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1457

Qy        1381 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1440
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Db        1458 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1517

Qy        1441 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1500
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Db        1518 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1577

Qy        1501 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1560
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Qy       1561 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1620
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Qy       1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740
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Qy       1741 CTCCCTACTTCCAAGAAAAATAATT-AAAAAAAAAACTTCATTCTAAACCAAAAAAAAAA 1799
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Qy       1800 AAAAA 1804
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RESULT 9
AX376004
LOCUS       AX376004                1879 bp    DNA     linear   PAT 01-MAR-2002
DEFINITION  Sequence 71 from Patent WO0168848.
ACCESSION   AX376004
VERSION     AX376004.1  GI:19170395
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Baker,K.P., Chen,J., Desnoyers,L., Goddard,A., Godowski,P.J.,
            Gurney,A.L., Pan,J., Smith,V., Watanabe,C.K., Wood,W.I. and
            Zhang,Z.
  TITLE     Secreted and transmembrane polypeptides and nucleic acids encoding
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  JOURNAL   Patent: WO 0168848-A 71 20-SEP-2001;
            Genentech, Inc. (US)
FEATURES             Location/Qualifiers
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ORIGIN
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  Query Match             98.9%;  Score 1784.4;  DB 6;  Length 1879;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1785;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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Qy         61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120
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Db        154 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 213

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Qy        241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300
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Db        334 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 393

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DEFINITION Homo sapiens clone DNA45493 BACE2 (UNQ418) mRNA, complete cds.
ACCESSION AY358927
VERSION AY358927.1 GI:37182971
KEYWORDS FLI_CDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1879)
AUTHORS Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J., Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B., Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E., Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S., Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C., Schoenfeld,J., Seshagiri,S., Simmons,L., Singh,J., Smith,V., Stinson,J., Vagts,A., Vandlen,R., Watanabe,C., Wieand,D., Woods,K., Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z., Goddard,A., Wood,W.I. and Godowski,P.
TITLE The Secreted Protein Discovery Initiative (SPDI), a Large-Scale Effort to Identify Novel Human Secreted and Transmembrane Proteins: A Bioinformatics Assessment
JOURNAL Genome Res. 13 (10), 2265-2270 (2003)
PUBMED 12975309
REFERENCE 2 (bases 1 to 1879)
AUTHORS Clark,H.F.
TITLE Direct Submission
JOURNAL Submitted (01-AUG-2003) Department of Bioinformatics, Genentech, Inc., 1 DNA Way, South San Francisco, CA 94080, USA
FEATURES Location/Qualifiers
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ESSLVRHRWK"

ORIGIN

Query Match 98.9%; Score 1784.4; DB 9; Length 1879;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1785; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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RESULT 11
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DEFINITION  Homo sapiens beta-site APP-cleaving enzyme 2, transcript variant a,
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ACCESSION   BC014453
VERSION     BC014453.1  GI:15680203
KEYWORDS    MGC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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REFERENCE   1  (bases 1 to 1864)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
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            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
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  TITLE     Generation and initial analysis of more than 15,000 full-length
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  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
  MEDLINE   22388257
   PUBMED   12477932
REFERENCE   2  (bases 1 to 1864)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-SEP-2001) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
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COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
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            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Genome Sequence Centre,
            BC Cancer Agency, Vancouver, BC, Canada
            info@bcgsc.bc.ca
            Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
            Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
            Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
            Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
            Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline
            Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott,
            Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
            George Yang, Scott Zuyderduyn, Marco Marra.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAL Plate: 34 Row: l Column: 22
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 21040358.
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(acid) proteases include pepsins, cathepsins, and renins. Two-domain structure, probably arising from ancestral duplication. This family does not include the retroviral nor retrotransposon proteases (pfam00077), which are much smaller and appear to be homologous to a single domain of the eukaryotic asp proteases"
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ORIGIN

Query Match 98.0%; Score 1768.2; DB 9; Length 1864;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1770; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy        481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540
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Qy        721 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 780
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DEFINITION  Metastatic breast and colon cancer regulated genes.
ACCESSION   BD231786
VERSION     BD231786.1  GI:33041556
KEYWORDS    JP 2002513542-A/18.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1873)
  AUTHORS   Xin,H. and Giese,K.
  TITLE     Metastatic breast and colon cancer regulated genes
  JOURNAL   Patent: JP 2002513542-A 18 14-MAY-2002;
            CHIRON CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002513542-A/18
            PD   14-MAY-2002
            PF   24-DEC-1998 JP 2000526659
            PR   31-DEC-1997 US    60/070112
            PI   HONG XIN,KLAUSE GIESE
            PC   C12N15/00,C07K14/47,C07K16/18,C07K19/00,C12N9/64,C12N15/09, PC
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Best Local Similarity 99.8%; Pred. No. 0;
Matches 1770; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db        401 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 460

Qy        361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420
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Qy        421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480
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Qy        481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540
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Qy        541 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600
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Qy        781 GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA 840
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Db       1061 GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC 1120

Qy       1021 CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC 1080
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Qy       1381 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1440
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Qy       1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740
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DEFINITION  Sequence 18 from patent US 6635748.
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VERSION     AR411231.1  GI:40163285
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1873)
  AUTHORS   Xin,H. and Giese,K.
  TITLE     Metastatic breast and colon cancer regulated genes
  JOURNAL   Patent: US 6635748-A 18 21-OCT-2003;
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match           98.0%;  Score 1768.2;  DB 6;  Length 1873;
  Best Local Similarity 99.8%;  Pred. No. 0;
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RESULT 14
AF117892
LOCUS       AF117892                1873 bp    mRNA    linear   PRI 14-JUL-2000
DEFINITION  Homo sapiens aspartic-like protease mRNA, complete cds.
ACCESSION   AF117892
VERSION     AF117892.1  GI:5565865
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1873)
  AUTHORS   Xin,H., Stephans,J.C., Duan,X., Harrowe,G., Kim,E., Grieshammer,U.,
            Kingsley,C. and Giese,K.
  TITLE     Identification of a novel aspartic-like protease differentially
            expressed in human breast cancer cell lines
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JOURNAL Biochim. Biophys. Acta 1501 (2-3), 125-137 (2000)
MEDLINE 20298348
PUBMED 10838186
REFERENCE 2 (bases 1 to 1873)
AUTHORS Xin,H., Stephans,J.C., Duan,X., Harrowe,G., Kim,E., Grieshammer,U. and Giese,K.
TITLE Direct Submission
JOURNAL Submitted (05-JAN-1999) Technologies, Chiron Co., 4560 Horton St., 4.5103, Emeryville, CA 94608, USA

FEATURES Location/Qualifiers
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ORIGIN

Query Match 98.0%; Score 1768.2; DB 9; Length 1873;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1770; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy          1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60
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Qy         61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120
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ACCESSION   AR136909
VERSION     AR136909.1  GI:14478159
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SOURCE      Unknown.
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REFERENCE   1  (bases 1 to 1862)
  AUTHORS   Powell,D.J., Southan,C., Chapman,C.G. and Evans,J.R.
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JOURNAL Patent: US 6162630-A 1 19-DEC-2000;

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ORIGIN

Query Match 97.9%; Score 1765.6; DB 6; Length 1862;
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Db        511 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 570

Qy        481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        571 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 630

Qy        541 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        631 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 690

Qy        601 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        691 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 750

Qy        661 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        751 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 810

Qy        721 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        811 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 870

Qy        781 GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        871 GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA 930

Qy        841 TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        931 TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC 990

Qy        901 ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        991 ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG 1050

Qy        961 GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1051 GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC 1110

Qy       1021 CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1111 CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC 1170

Qy       1081 TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1140
              |||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||
Db       1171 TACCTGAGAGACGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1230

Qy       1141 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1231 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA 1290

Qy       1201 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1291 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC 1350

Qy       1261 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1351 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1410

Qy       1321 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1411 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1470

Qy       1381 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1471 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1530

Qy       1441 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1531 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1590

Qy       1501 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1591 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1650
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Qy       1561 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1651 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1710

Qy       1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1711 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1770

Qy       1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1771 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1830

Qy       1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAA 1772
             |||||||||||||||||||  ||  |||||||
Db       1831 CTCCCTACTTCCAAGAAAAAAAAAAAAAAAA 1862
```

Search completed: March 5, 2004, 23:18:56
Job time : 6904 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: March 5, 2004, 16:24:13 ; Search time 701 Seconds
(without alignments)
10932.595 Million cell updates/sec

Title: US-09-668-314C-1
Perfect score: 1804
Sequence: 1 atgggcgcactggcccgggc.....aaaccaaaaaaaaaaaaaaa 1804

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_29Jan04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002s:*
7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1804	100.0	1804	3	AAA15661	Aaa15661 Human asp
2	1804	100.0	1804	4	AAS11701	Aas11701 DNA encod
3	1804	100.0	1804	4	AAD17864	Aad17864 Human asp
4	1804	100.0	1804	4	AAD13020	Aad13020 Human asp
5	1804	100.0	1804	4	AAD06738	Aad06738 Human asp
6	1804	100.0	1804	4	AAS11516	Aas11516 Human cDN
7	1804	100.0	1804	6	ABL52456	Abl52456 Human Asp

8	1784.4	98.9	1879	2	AAZ34056	Aaz34056 Human PRO
9	1784.4	98.9	1879	3	AAC78500	Aac78500 Human PRO
10	1784.4	98.9	1879	4	AAS45960	Aas45960 Human DNA
11	1784.4	98.9	1879	7	ABX78563	Abx78563 Human PRO
12	1784.4	98.9	1879	7	ACA75535	Aca75535 Novel hum
13	1784.4	98.9	1879	7	ACA71015	Aca71015 Human sec
14	1784.4	98.9	1879	7	ACC87543	Acc87543 Human sec
15	1784.4	98.9	1879	7	ACC86929	Acc86929 Human sec
16	1784.4	98.9	1879	7	ACD04102	Acd04102 Human sec
17	1784.4	98.9	1879	7	ACA69433	Aca69433 cDNA enco
18	1784.4	98.9	1879	7	ACA90278	Aca90278 Novel hum
19	1784.4	98.9	1879	7	ACC89385	Acc89385 Human sec
20	1784.4	98.9	1879	7	ACA98176	Aca98176 Novel hum
21	1784.4	98.9	1879	7	ACA93818	Aca93818 Human sec
22	1784.4	98.9	1879	7	ACD15211	Acd15211 Human sec
23	1784.4	98.9	1879	7	ACD08798	Acd08798 Human sec
24	1784.4	98.9	1879	7	ACC96718	Acc96718 Human sec
25	1784.4	98.9	1879	7	ACF15439	Acf15439 Human sec
26	1784.4	98.9	1879	7	ACD42589	Acd42589 Novel hum
27	1784.4	98.9	1879	7	ACA72806	Aca72806 Human PRO
28	1784.4	98.9	1879	7	ACD02978	Acd02978 Novel hum
29	1784.4	98.9	1879	7	ACD01793	Acd01793 Novel hum
30	1784.4	98.9	1879	7	ACA91985	Aca91985 Novel hum
31	1784.4	98.9	1879	7	ACA63624	Aca63624 Novel hum
32	1784.4	98.9	1879	7	ACA89410	Aca89410 cDNA enco
33	1784.4	98.9	1879	7	ACA73420	Aca73420 Human sec
34	1784.4	98.9	1879	7	ACA05735	Aca05735 Human sec
35	1784.4	98.9	1879	7	ACA66569	Aca66569 cDNA enco
36	1784.4	98.9	1879	7	ACF20144	Acf20144 Human sec
37	1784.4	98.9	1879	7	ACF19530	Acf19530 Human sec
38	1784.4	98.9	1879	7	ACD21818	Acd21818 Human sec
39	1784.4	98.9	1879	7	ACF12983	Acf12983 Human sec
40	1784.4	98.9	1879	7	ACD25086	Acd25086 Human sec
41	1784.4	98.9	1879	7	ACF00135	Acf00135 Human sec
42	1784.4	98.9	1879	7	ACA72192	Aca72192 Novel hum
43	1784.4	98.9	1879	7	ACD04716	Acd04716 Novel hum
44	1784.4	98.9	1879	7	ACD18177	Acd18177 Human sec
45	1784.4	98.9	1879	7	ACD08184	Acd08184 Human sec

ALIGNMENTS

RESULT 1
AAA15661
ID AAA15661 standard; cDNA; 1804 BP.
XX
AC AAA15661;
XX
DT 03-AUG-2000 (first entry)
XX
DE Human aspartyl protease 1 (Asp1) nucleotide sequence.
XX
KW Aspartyl protease; aspartase; amyloid precursor protein; APP; Asp 1;
KW Alzheimer's disease; beta secretase site; ss.
XX
OS Homo sapiens.

XX
PN WO200017369-A2.
XX
PD 30-MAR-2000.
XX
PF 23-SEP-1999; 99WO-US020881.
XX
PR 24-SEP-1998; 98US-0101594P.
XX
PA (PHAA) PHARMACIA & UPJOHN CO.
XX
PI Gurney ME, Bienkowski MJ, Heinrikson RL, Parodi LA, Yan R;
XX
DR WPI; 2000-303209/26.
DR P-PSDB; AAY88424.
XX
PT New enzyme designated human aspartase useful in research into Alzheimer's
PT Disease is capable of cleaving amyloid protein precursor at the beta
PT secretase site to produce amyloid beta peptide.
XX
PS Claim 11; Fig 1; 183pp; English.
XX
CC This sequence represents the human aspartyl protease nucleotide sequence.
CC The invention relates to a protease capable of cleaving the beta
CC secretase site of amyloid precursor protein (APP). The protease contains
CC a sequence encoding the amino acid sequence DTG and a sequence encoding
CC DSG or DTG separated by 100-300 amino acids. When mutated the APP gene
CC causes an autosomal dominant form of Alzheimer's disease. APP localises
CC to the cell surface membrane and have a single C-terminal transmembrane
CC domain. Proteolytic processing of APP produces the amyloid beta protein,
CC which is possibly very important in Alzheimer's disease. The invention
CC includes a nucleotide sequence encoding the protease, a vector containing
CC the nucleotide sequence, and a cell line comprising the vector. Methods
CC for screening for inhibitors of beta secretase activity are also given in
CC the invention. The human aspartase protein and nucleotide sequences and
CC the methods for identifying inhibitors of the protease, are useful in the
CC treatment of and research in to Alzheimer's disease
XX
SQ Sequence 1804 BP; 397 A; 520 C; 458 G; 429 T; 0 U; 0 Other;

Query Match 100.0%; Score 1804; DB 3; Length 1804;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1804; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60

Qy         61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120

Qy        121 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180

Qy        181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240
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Db        181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240

Qy        241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300

Qy        301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360

Qy        361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420

Qy        421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480

Qy        481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540

Qy        541 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600

Qy        601 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 660

Qy        661 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 720

Qy        721 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 780

Qy        781 GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA 840

Qy        841 TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC 900

Qy        901 ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG 960

Qy        961 GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC 1020

Qy       1021 CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        1021 CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC 1080

Qy        1081 TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1140
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1081 TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1140

Qy        1141 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA 1200
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1141 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA 1200

Qy        1201 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC 1260
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1201 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC 1260

Qy        1261 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1320
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1261 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1320

Qy        1321 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1380
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1321 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1380

Qy        1381 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1440
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1381 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1440

Qy        1441 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1500
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1441 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1500

Qy        1501 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1560
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1501 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1560

Qy        1561 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1620
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1561 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1620

Qy        1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1680
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1680

Qy        1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740

Qy        1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAAACCAAAAAAAAAAA 1800
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAAACCAAAAAAAAAAA 1800

Qy        1801 AAAA 1804
               ||||
Db        1801 AAAA 1804
```

RESULT 2
AAS11701

ID AAS11701 standard; DNA; 1804 BP.
XX
AC AAS11701;
XX
DT 24-OCT-2001 (first entry)
XX
DE DNA encoding human aspartyl protease 1 (Asp-1).
XX
KW Human; aspartyl protease 1; Asp-1; nootropic; neuroprotective;
KW aspartyl protease 2; Asp2; amyloid protein precursor; APP;
KW beta-secretase; Alzheimer's disease; ds.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT CDS   1. .1557
FT   /*tag= a
FT   /product= "Aspartyl protease-1 (Asp-1)"
XX
PN WO200149097-A2.
XX
PD 12-JUL-2001.
XX
PF 09-MAY-2001; 2001WO-IB000797.
XX
PR 09-MAY-2001; 2001WO-IB000797.
XX
PA (BIEN/) BIENKOWSKI M J.
PA (GURN/) GURNEY M E.
PA (HEIN/) HEINRIKSON R L.
PA (PARO/) PARODI L A.
PA (YANR/) YAN R.
XX
PI Bienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;
XX
DR WPI; 2001-502548/55.
DR P-PSDB; AAU07201.
XX
PT Novel purified polypeptide comprising fragment of mammalian aspartyl
PT protease 2, lacking Asp2 transmembrane domain and retaining beta
PT secretase activity of Asp2 useful for identifying inhibitors of Asp2
PT activity.
XX
PS Example 2; Fig 1; 185pp; English.
XX
CC The invention relates to a novel purified polypeptide comprising a
CC fragment of mammalian aspartyl protease 2 (Asp2) protein which lacks the
CC Asp2 transmembrane domain and the Asp2 protein, and where the polypeptide
CC and the fragment retain the beta-secretase activity of the mammalian Asp2
CC protein. Also included is an isoform of amyloid protein precursor (APP)
CC comprising the amino acid sequence of a APP or its fragment containing an
CC APP cleavage site recognisable by a mammalian beta-secretase, and further
CC comprising two lysine residues at the carboxyl terminus of the amino acid
CC sequence of the mammalian APP or APP fragment. The polypeptides are used
CC for assaying for modulators of beta-secretase activity; identifying
CC agents that inhibit the APP processing activity of human Asp2 aspartyl
CC protease (Hu-Asp2); identifying agents that modulate the activity of Asp2

CC ; and for reducing cellular production of amyloid beta (Abeta) from APP.
CC Agents identified by the above methods are useful for treating
CC Alzheimer's disease; and for identifying modulators of amyloid-beta
CC (Abeta) peptide production, for use in designing therapeutics for the
CC treatment or prevention of Alzheimer's disease. Probes and primers
CC derived from Asp nucleic acid sequences are useful for detecting Hu-Asp
CC nucleic acids in in vitro assays and in Northern and Southern blots. The
CC present sequence represents the coding sequence of human Asp-1
XX
SQ Sequence 1804 BP; 397 A; 520 C; 458 G; 429 T; 0 U; 0 Other;

Query Match 100.0%; Score 1804; DB 4; Length 1804;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1804; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60

Qy         61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120

Qy        121 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180

Qy        181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240
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Qy        241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300
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Qy        301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360
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Qy        361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420
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Qy        421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480
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Db        421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480

Qy        481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540
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Db        601 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 660

Qy        661 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 720
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Qy        721 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        781 GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA 840
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Db        961 GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC 1020

Qy       1021 CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC 1080
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Db       1021 CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC 1080

Qy       1081 TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1140
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Qy       1141 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA 1200
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Qy       1321 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1380
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Qy       1381 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1440
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Qy       1501 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1560
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Db       1501 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1560

Qy       1561 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1620
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Qy       1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAAACCAAAAAAAAAAA 1800
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Qy       1801 AAAA 1804
              ||||
Db       1801 AAAA 1804
```

```
RESULT 3
AAD17864
ID   AAD17864 standard; cDNA; 1804 BP.
XX
AC   AAD17864;
XX
DT   10-DEC-2001  (first entry)
XX
DE   Human aspartyl protease 1 (hu-Asp1) cDNA.
XX
KW   Human; aspartyl protease 1; Asp1; amyloid precursor protein; APP;
KW   Alzheimer's disease; AD; dementia; neurofibrillary tangle; gliosis;
KW   amyloid plaque; neuronal loss; proteolytic; nootropic; neuroprotective;
KW   chromosome 21; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
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FT                   /product= "Human aspartyl protease 1"
FT   sig_peptide     1. .60
FT                   /*tag=  b
FT   mat_peptide     61. .1554
FT                   /*tag=  c
FT                   /product= "Mature human aspartyl protease 1"
XX
PN   GB2357767-A.
XX
PD   04-JUL-2001.
XX
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PF 22-SEP-2000; 2000GB-00023315.
XX
PR 23-SEP-1999; 99US-00404133.
PR 23-SEP-1999; 99US-0155493P.
PR 23-SEP-1999; 99WO-US020881.
PR 13-OCT-1999; 99US-00416901.
PR 06-DEC-1999; 99US-0169232P.
XX
PA (PHAA) PHARMACIA & UPJOHN CO.
XX
PI Bienkowkski MJ, Gurney M;
XX
DR WPI; 2001-444208/48.
DR P-PSDB; AAE10628.
XX
PT Polypeptide comprising fragments of human aspartyl protease with amyloid
PT precursor protein processing activity and alpha-secretase activity, for
PT identifying modulators useful in treating Alzheimer's disease.
XX
PS Claim 30; Fig 1; 187pp; English.
XX
CC The patent discloses human aspartyl protease 1 (hu-Asp1) or modified Asp1
CC proteins which lack transmembrane domain or amino terminal domain or
CC cytoplasmic domain and retains alpha-secretase activity and amyloid
CC protein precursor (APP) processing activity. The proteins of the
CC invention are useful for assaying hu-Asp1 alpha-secretase activity, which
CC in turn is useful for identifying modulators of hu-Asp1 alpha-secretase
CC activity, where modulators that increase hu-Asp1 alpha-secretase activity
CC are useful for treating Alzheimer's disease (AD) which causes progressive
CC dementia with consequent formation of amyloid plaques, neurofibrillary
CC tangles, gliosis and neuronal loss. Hu-Asp1 protease substrate is useful
CC for assaying hu-Asp1 proteolytic activity, by contacting hu-Asp1 protein
CC with the substrate under acidic conditions and determining the level of
CC hu-Asp1 proteolytic activity. The present sequence is a cDNA encoding
CC human Asp1 protein. Asp1 gene is localised on chromosome 21
XX
SQ Sequence 1804 BP; 397 A; 520 C; 458 G; 429 T; 0 U; 0 Other;

Query Match 100.0%; Score 1804; DB 4; Length 1804;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1804; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60
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Db          1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60

Qy         61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120
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Db         61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120

Qy        121 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180

Qy        181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240
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Qy        241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300
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Qy        301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360
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Qy        361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420
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Qy        421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480
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Db        421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480

Qy        481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        541 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600
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Db        541 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600

Qy        601 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 660

Qy        661 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 720
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Db        661 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 720

Qy        721 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 780
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Qy        781 GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA 840
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Db       1021 CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC 1080
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Qy       1081 TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1140
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Qy       1441 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1500
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Qy       1501 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1560
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Db       1501 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1560

Qy       1561 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1620
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Qy       1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740
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Db       1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740

Qy       1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAAACCAAAAAAAAAAA 1800
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Qy       1801 AAAA 1804
              ||||
Db       1801 AAAA 1804
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RESULT 4
AAD13020
ID   AAD13020 standard; cDNA; 1804 BP.
XX

AC AAD13020;
XX
DT 23-OCT-2001 (first entry)
XX
DE Human aspartyl protease 1 (Hu-Asp1) cDNA.
XX
KW Human; aspartyl protease 1; Asp 1; beta-amyloid precursor protein; APP;
KW beta-secretase; Alzheimer's disease; dementia; amyloid plaque; gliosis;
KW neurofibrillary tangle; neuronal loss; amyloid-beta peptide; nootropic;
KW neuroprotective; antisense therapy; gene therapy; chromosome 21; ss.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
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FT   /product= "Human aspartyl protease 1 (Hu-Asp1)"
FT sig_peptide   1. .60
FT   /*tag= b
FT mat_peptide   61. .1554
FT   /*tag= c
FT   /product= "Mature human aspartyl protease 1 (Hu-Asp1)"
XX
PN WO200150829-A2.
XX
PD 19-JUL-2001.
XX
PF 09-MAY-2001; 2001WO-IB000799.
XX
PR 09-MAY-2001; 2001WO-IB000799.
XX
PA (BIEN/) BIENKOWSKI M J.
PA (GURN/) GURNEY M E.
PA (HEIN/) HEINRIKSON R L.
PA (PARO/) PARODI L A.
PA (YANR/) YAN R.
XX
PI Bienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;
XX
DR WPI; 2001-483072/52.
DR P-PSDB; AAE06858.
XX
PT Novel purified polypeptide comprising fragment of mammalian aspartyl
PT protease 2, lacking Asp2 transmembrane domain and retaining beta
PT secretase activity of Asp2 useful for identifying inhibitors of Asp2
PT activity.
XX
PS Example 2; Fig 1; 185pp; English.
XX
CC The invention relates to human aspartyl proteases (Hu-Asp), beta-amyloid
CC precursor protein (APP) isoforms and their corresponding DNA molecules.
CC Human aspartyl proteases can act as beta-secretase proteases useful for
CC treating Alzheimer's disease. APP isoforms are useful for identifying
CC modulators of amyloid-beta peptide production, for use in designing
CC therapeutics for the treatment and prevention of Alzheimer's disease,
CC dementia, formation of amyloid plaques, neurofibrillary tangles, gliosis
CC and neuronal loss. APP isoforms are also used in methods for identifying

CC inhibitors and modulators of human Asp2 activity. The invention relates
CC to a method for identifying agents that modulate the activity of human
CC aspartyl protease Asp2. Amyloid-beta peptides obtained from APP are used
CC as a means to screen in cellular assays for the inhibitors of beta- and
CC gamma- secretase. Hu-Asp DNA fragments are useful as probes or primers in
CC polymerase chain reactions (PCR). The probes are useful for detecting Hu-
CC Asp nucleic acids in in vitro assays and in Northern and Southern blots.
CC The present cDNA sequence encodes human aspartyl protease 1 (Hu-Asp1). Hu
CC -Asp 1 gene is localised on chromosome 21
XX
SQ Sequence 1804 BP; 397 A; 520 C; 458 G; 429 T; 0 U; 0 Other;

Query Match 100.0%; Score 1804; DB 4; Length 1804;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1804; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60
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Db          1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60

Qy         61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120

Qy        121 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180

Qy        181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300
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Qy        301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360

Qy        361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420

Qy        421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480

Qy        481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540
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Qy        541 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600
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Qy        601 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 660
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Db        601 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 660

Qy        661 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 720

Db        661 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 720

Qy        721 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 780

Db        721 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 780

Qy        781 GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA 840

Db        781 GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA 840

Qy        841 TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC 900

Db        841 TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC 900

Qy        901 ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG 960

Db        901 ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG 960

Qy        961 GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC 1020

Db        961 GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC 1020

Qy       1021 CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC 1080

Db       1021 CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC 1080

Qy       1081 TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1140

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Db       1141 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA 1200

Qy       1201 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC 1260

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Qy       1261 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1320

Db       1261 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1320

Qy       1321 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1380

Db       1321 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1380

Qy       1381 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1440

Db       1381 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1440

Qy       1441 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1500
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Db        1441 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1500

Qy        1501 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1560
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1501 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1560

Qy        1561 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1620
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1680
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1680

Qy        1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740

Qy        1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAAACCAAAAAAAAAAA 1800
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAAACCAAAAAAAAAAA 1800

Qy        1801 AAAA 1804
               ||||
Db        1801 AAAA 1804


RESULT 5
AAD06738
ID   AAD06738 standard; cDNA; 1804 BP.
XX
AC   AAD06738;
XX
DT   10-AUG-2001  (first entry)
XX
DE   Human aspartyl protease 1 (Asp 1) cDNA.
XX
KW   Human; alpha-secretase; amyloid precursor protein; APP; therapy;
KW   Alzheimer's disease; antialzheimer's; aspartyl protease 1; Asp 1;
KW   beta-secretase; chromosome 21; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
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FT   sig_peptide     1. .60
FT                   /*tag=  b
FT   sig_peptide     64. .186
FT                   /*tag=  c
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FT                   /*tag=  d
FT                   /note= "Pro-peptide"
FT   mat_peptide     187. .1554
FT                   /*tag=  e
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XX
PN   WO200123533-A2.
XX
PD   05-APR-2001.
XX
PF   22-SEP-2000; 2000WO-US026080.
XX
PR   23-SEP-1999;   99US-0155493P.
PR   23-SEP-1999;   99WO-US020881.
PR   13-OCT-1999;   99US-00416901.
PR   06-DEC-1999;   99US-0169232P.
XX
PA   (PHAA) PHARMACIA & UPJOHN CO.
XX
PI   Gurney M, Bienkowski MJ;
XX
DR   WPI; 2001-290516/30.
DR   P-PSDB; AAE02580.
XX
PT   Enzymes that cleave the alpha-secretase site of the amyloid precursor
PT   protein, useful for the treatment of Alzheimer's disease.
XX
PS   Example 2; Fig 1; 189pp; English.
XX
CC   The present invention relates to enzymes for cleaving the alpha-
CC   secretase site of the amyloid precursor protein (APP) and methods of
CC   identifying those enzymes. The methods may be used to identify enzymes
CC   that may be used to cleave the alpha-secretase cleavage site of the APP
CC   protein. The enzymes may be used to treat or modulate the progress of
CC   Alzheimer's disease. The present sequence is human aspartyl protease 1
CC   (Asp 1) cDNA. Asp 1 has alpha-secretase protease and beta-secretase
CC   protease activities. Asp 1 gene is located on chromosome 21
XX
SQ   Sequence 1804 BP; 397 A; 520 C; 458 G; 429 T; 0 U; 0 Other;

Query Match   100.0%; Score 1804; DB 4; Length 1804;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1804; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy          1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60

Qy         61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120

Qy        121 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180

Qy        181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300
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Db        241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300

Qy        301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360

Db        301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360

Qy        361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420

Db        361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420

Qy        421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480

Db        421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480

Qy        481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540

Db        481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540

Qy        541 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600

Db        541 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600

Qy        601 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 660

Db        601 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 660

Qy        661 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 720

Db        661 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 720

Qy        721 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 780

Db        721 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 780

Qy        781 GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA 840

Db        781 GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA 840

Qy        841 TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC 900

Db        841 TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC 900

Qy        901 ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG 960

Db        901 ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG 960

Qy        961 GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC 1020

Db        961 GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC 1020

Qy       1021 CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC 1080

Db       1021 CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC 1080

Qy       1081 TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1140
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Db        1081 TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1140

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               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1141 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA 1200

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               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        1261 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1320
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Qy        1321 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1380
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Qy        1381 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1440
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Qy        1441 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1500
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Db        1441 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1500

Qy        1501 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1560
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Qy        1561 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1620
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Db        1561 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1620

Qy        1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1680
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740
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Qy        1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAAACCAAAAAAAAAAA 1800
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Db        1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAAACCAAAAAAAAAAA 1800

Qy        1801 AAAA 1804
               ||||
Db        1801 AAAA 1804


RESULT 6
AAS11516
ID   AAS11516 standard; cDNA; 1804 BP.
XX
AC   AAS11516;
XX
```

DT 24-OCT-2001 (first entry)
XX
DE Human cDNA encoding Aspartyl protease 1 (Asp1).
XX
KW Human; Aspartyl protease; Asp1; Asp2; beta-secretase; nootropic;
KW neuroprotective; amyloid protein precursor; APP; Alzheimer's disease;
KW amyloid-beta; Abeta; ss.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT CDS   1. .1557
FT   /*tag= a
FT   /product= "Asp1"
XX
PN WO200149098-A2.
XX
PD 12-JUL-2001.
XX
PF 09-MAY-2001; 2001WO-IB000798.
XX
PR 09-MAY-2001; 2001WO-IB000798.
XX
PA (BIEN/) BIENKOWSKI M J.
PA (GURN/) GURNEY M E.
PA (HEIN/) HEINRIKSON R L.
PA (PARO/) PARODI L A.
PA (YANR/) YAN R.
XX
PI Bienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;
XX
DR WPI; 2001-502549/55.
DR P-PSDB; AAU06602.
XX
PT Novel purified polypeptide comprising fragment of mammalian aspartyl
PT protease 2, lacking Asp2 transmembrane domain and retaining beta
PT secretase activity of Asp2 useful for identifying inhibitors of Asp2
PT activity.
XX
PS Example 2; Fig 1; 185pp; English.
XX
CC The invention relates to a purified polypeptide comprising a fragment of
CC mammalian aspartyl protease (Asp)2 protein which lacks the Asp2
CC transmembrane domain and the Asp2 protein, and where the polypeptide and
CC the fragment retain the beta-secretase activity of the mammalian Asp2
CC protein. The invention also details polynucleotides for the Asp proteins
CC and vectors expressing them, and a polypeptide (isoform of amyloid
CC protein precursor (APP)) comprising the amino acid sequence of an APP or
CC its fragment containing an APP cleavage site recognizable by a mammalian
CC beta-secretase, and further comprising two lysine residues at the
CC carboxyl terminus of the amino acid sequence of the mammalian APP or APP
CC fragment. Also included in the invention are methods of identifying
CC modulators or inhibitors of Asp2. Modulators and inhibitors of Asp2 are
CC useful for treating Alzheimer's disease. APP is useful in methods for
CC identifying inhibitors or modulators of human Asp2 activity and amyloid-
CC beta (Abeta) peptide production. APP is also useful in designing
CC therapeutics for the treatment or prevention of Alzheimer's disease. APP

CC comprising the APP-Sw-beta-secretase peptide sequence (NLDA), which is
CC associated with increased levels of Abeta processing is useful in assays
CC relating the Alzheimer's research. The expression vector is useful for
CC recombinantly expressing APP. Nucleic acids that hybridise to Asp
CC oligonucleotides are useful as probes or primers. The probes are useful
CC for detecting Hu-Asp nucleic acids in in vitro assays and in Northern and
CC Southern blots. The present sequence encodes human Asp1
XX
SQ Sequence 1804 BP; 397 A; 520 C; 458 G; 429 T; 0 U; 0 Other;

Query Match 100.0%; Score 1804; DB 4; Length 1804;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1804; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60
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Db          1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60

Qy         61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120

Qy        121 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180

Qy        181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240

Qy        241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300

Qy        301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360

Qy        361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420

Qy        421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480

Qy        481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540

Qy        541 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600

Qy        601 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 660
```

```
Qy        661 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 720

Qy        721 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 780

Qy        781 GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA 840

Qy        841 TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC 900

Qy        901 ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG 960
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Db        901 ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG 960

Qy        961 GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC 1020

Qy       1021 CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC 1080

Qy       1081 TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1140
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Db       1081 TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1140

Qy       1141 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA 1200

Qy       1201 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC 1260

Qy       1261 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1320

Qy       1321 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1380

Qy       1381 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1440
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Db       1381 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1440

Qy       1441 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1500
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Qy       1501 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1560

Qy       1561 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1620

Qy       1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1680

Qy       1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740

Qy       1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAAACCAAAAAAAAAAA 1800
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAAACCAAAAAAAAAAA 1800

Qy       1801 AAAA 1804
              ||||
Db       1801 AAAA 1804
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```
RESULT 7
ABL52456
ID   ABL52456 standard; cDNA; 1804 BP.
XX
AC   ABL52456;
XX
DT   16-JUL-2002  (first entry)
XX
DE   Human Asp-1 nucleotide sequence SEQ ID NO:1.
XX
KW   Human; Asp-1; Asp-2; aspartyl protease; enzyme; Alzheimer's disease;
KW   proteolytic; chromosome 21; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1557
FT                   /*tag=  a
FT                   /product= "Asp-1"
FT                   /note= "aspartyl protease"
XX
PN   GB2367060-A.
XX
PD   27-MAR-2002.
XX
PF   29-OCT-2001; 2001GB-00025934.
XX
PR   23-SEP-1999;   99US-00404133.
PR   23-SEP-1999;   99US-0155493P.
PR   23-SEP-1999;   99WO-US020881.
PR   13-OCT-1999;   99US-00416901.
PR   06-DEC-1999;   99US-0169232P.
```

PR 22-SEP-2000; 2000GB-00023315.
XX
PA (PHAA) PHARMACIA & UPJOHN CO.
XX
PI Bienkowkski MJ, Gurney M;
XX
DR WPI; 2002-397167/43.
DR P-PSDB; ABB78589.
XX
PT Human aspartyl protease 1 substrates useful in assays to detect aspartyl
PT protease activity, e.g. for the diagnosis of Alzheimer's disease.
XX
PS Claim 8; Fig 1; 182pp; English.
XX
CC The present invention describes a human aspartyl protease 1 (hu-Asp1)
CC substrate (I) which comprises a peptide of no more than 50 amino acids,
CC and which comprises the 8 amino acid sequence Gly-Leu-Ala-Leu-Ala-Leu-
CC Glu-Pro. Also described are: (1) a method (II) for assaying hu-Asp1
CC proteolytic activity, comprising: (a) contacting a hu-Asp1 protein with
CC (I) under acidic conditions; and (b) determining the level of hu-Asp1
CC proteolytic activity; (2) a purified polynucleotide (III) comprising a
CC nucleotide sequence that hybridises under stringent conditions to the non
CC -coding strand complementary to a defined 1804 nucleotide sequence (see
CC ABL52456) where the nucleotide sequence encodes a polypeptide having Asp1
CC proteolytic activity and lacks nucleotides encoding a transmembrane
CC domain); (3) a purified polynucleotide (III') comprising a sequence that
CC hybridises under stringent conditions to (III) (the nucleotide sequence
CC encodes a polypeptide further lacking a pro-peptide domain corresponding
CC to amino acids 23-62 of hu-Asp1 (see ABB78589)); (4) a vector (IV)
CC comprising (III) or (III'); and (5) a host cell (V) transformed or
CC transfected with (III), (III') and/or (IV). The hu-Asp1 protease
CC substrate (I) may be used as an enzyme substrate in assays to detect
CC aspartyl protease activity, (II) and therefore diagnose diseases
CC associated with aberrant hu-Asp1 expression and activity such as
CC Alzheimer's disease. Hu-Asp1 has been localised to chromosome 21, while
CC hu-Asp2 has been localised to chromosome 11q23.3-24.1. The present
CC sequence encodes hu-Asp1 from the present invention
XX
SQ Sequence 1804 BP; 397 A; 520 C; 458 G; 429 T; 0 U; 0 Other;

Query Match 100.0%; Score 1804; DB 6; Length 1804;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1804; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60

Qy         61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120

Qy        121 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180

Qy        181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240
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Db        181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240

Qy        241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300
Db        241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300

Qy        301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360
Db        301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360

Qy        361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420
Db        361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420

Qy        421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480
Db        421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480

Qy        481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540
Db        481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540

Qy        541 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600
Db        541 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600

Qy        601 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 660
Db        601 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 660

Qy        661 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 720
Db        661 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 720

Qy        721 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 780
Db        721 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 780

Qy        781 GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA 840
Db        781 GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA 840

Qy        841 TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC 900
Db        841 TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC 900

Qy        901 ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG 960
Db        901 ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG 960

Qy        961 GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC 1020
Db        961 GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC 1020

Qy       1021 CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC 1080
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Db        1021 CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC 1080

Qy        1081 TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1140
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Db        1081 TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1140

Qy        1141 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA 1200
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Db        1141 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA 1200

Qy        1201 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC 1260
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1201 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC 1260

Qy        1261 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1320
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Qy        1321 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1380
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Db        1321 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1380

Qy        1381 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1440
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Db        1381 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1440

Qy        1441 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1500
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1441 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1500

Qy        1501 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1560
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1501 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1560

Qy        1561 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1620
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Db        1561 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1620

Qy        1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1680
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Db        1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1680

Qy        1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740
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Db        1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740

Qy        1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAAACCAAAAAAAAAAA 1800
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Qy        1801 AAAA 1804
               ||||
Db        1801 AAAA 1804
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RESULT 8
AAZ34056

ID AAZ34056 standard; cDNA; 1879 BP.
XX
AC AAZ34056;
XX
DT 07-DEC-1999 (first entry)
XX
DE Human PRO852 nucleotide sequence.
XX
KW Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;
KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;
KW secreted protein; transmembrane protein; ss.
XX
OS Homo sapiens.
XX
PN WO9946281-A2.
XX
PD 16-SEP-1999.
XX
PF 08-MAR-1999; 99WO-US005028.
XX
PR 10-MAR-1998; 98US-0077450P.
PR 11-MAR-1998; 98US-0077632P.
PR 11-MAR-1998; 98US-0077641P.
PR 11-MAR-1998; 98US-0077649P.
PR 12-MAR-1998; 98US-0077791P.
PR 13-MAR-1998; 98US-0078004P.
PR 17-MAR-1998; 98US-00040220.
PR 20-MAR-1998; 98US-0078886P.
PR 20-MAR-1998; 98US-0078910P.
PR 20-MAR-1998; 98US-0078936P.
PR 20-MAR-1998; 98US-0078939P.
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PR 27-MAR-1998; 98US-0079664P.
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PR 27-MAR-1998; 98US-0079728P.
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PR 31-MAR-1998; 98US-0080107P.
PR 31-MAR-1998; 98US-0080165P.
PR 31-MAR-1998; 98US-0080194P.
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PR 01-APR-1998; 98US-0080328P.
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PR 22-APR-1998; 98US-0082704P.
PR 22-APR-1998; 98US-0082804P.
PR 23-APR-1998; 98US-0082767P.
PR 23-APR-1998; 98US-0082796P.
PR 27-APR-1998; 98US-0083336P.
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PR 30-APR-1998; 98US-0083742P.
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PR 06-MAY-1998; 98US-0084414P.
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PR 07-MAY-1998; 98US-0084639P.
PR 07-MAY-1998; 98US-0084640P.
PR 07-MAY-1998; 98US-0084643P.
PR 13-MAY-1998; 98US-0085323P.
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PR 15-MAY-1998; 98US-0085580P.
PR 15-MAY-1998; 98US-0085582P.
PR 15-MAY-1998; 98US-0085689P.
PR 15-MAY-1998; 98US-0085697P.
PR 15-MAY-1998; 98US-0085700P.
PR 15-MAY-1998; 98US-0085704P.
PR 18-MAY-1998; 98US-0086023P.
PR 22-MAY-1998; 98US-0086392P.
PR 22-MAY-1998; 98US-0086414P.
PR 22-MAY-1998; 98US-0086430P.
PR 22-MAY-1998; 98US-0086486P.
PR 28-MAY-1998; 98US-0087098P.
PR 28-MAY-1998; 98US-0087106P.
PR 28-MAY-1998; 98US-0087208P.
PR 30-JUL-1998; 98US-0094651P.
PR 11-SEP-1998; 98US-0100038P.
XX
PA (GETH) GENENTECH INC.
XX
PI Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;
XX
DR WPI; 1999-551358/46.

DR P-PSDB; AAY41714.
XX
PT New secreted and transmembrane polypeptides and their polynucleotides,
PT useful for treating blood coagulation disorders, cancers and cellular
PT adhesion disorders.
XX
PS Claim 2; Fig 72; 530pp; English.
XX
CC The present invention describes secreted and transmembrane polypeptides
CC and their polynucleotides. The nucleotide sequences are useful as sources
CC of probes, primers, for chromosome mapping, and for generation of
CC antisense sequences. They can also be used to create transgenic animals.
CC The proteins can be used to treat a variety of diseases and disorders,
CC depending on their function. Diseases that may be treated include blood
CC coagulation disorders, cancers and cellular adhesion disorders. They may
CC also be used to raise antibodies. AAZ33891 to AAZ34338, and AAY41685 to
CC AAY41774 represent polynucleotide and polypeptide sequence given in the
CC exemplification of the present invention
XX
SQ Sequence 1879 BP; 388 A; 559 C; 498 G; 434 T; 0 U; 0 Other;

Query Match 98.9%; Score 1784.4; DB 2; Length 1879;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1785; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         94 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 153

Qy         61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        154 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 213

Qy        121 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        214 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 273

Qy        181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        274 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 333

Qy        241 GTAGACAACCTGCAGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        334 GTAGACAACCTGCAGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 393

Qy        301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        394 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 453

Qy        361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        454 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 513

Qy        421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        514 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 573
```

```
Qy        481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        574 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 633

Qy        541 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        634 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 693

Qy        601 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        694 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 753

Qy        661 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        754 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 813

Qy        721 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        814 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 873

Qy        781 GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        874 GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA 933

Qy        841 TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        934 TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC 993

Qy        901 ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        994 ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG 1053

Qy        961 GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1054 GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC 1113

Qy       1021 CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1114 CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC 1173

Qy       1081 TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1140
              |||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||
Db       1174 TACCTGAGAGACGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1233

Qy       1141 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1234 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA 1293

Qy       1201 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1294 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC 1353

Qy       1261 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1354 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1413

Qy       1321 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1380
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                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1414 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1473

Qy        1381 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1440
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1474 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1533

Qy        1441 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1500
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1534 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1593

Qy        1501 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1560
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1594 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1653

Qy        1561 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1620
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1654 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1713

Qy        1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1680
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1714 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1773

Qy        1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1774 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1833

Qy        1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAA 1786
                    ||||||||||||||||||||||||||||||||||||||||||||
Db        1834 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAA 1879
```

```
RESULT 9
AAC78500
ID   AAC78500 standard; cDNA; 1879 BP.
XX
AC   AAC78500;
XX
DT   08-FEB-2001  (first entry)
XX
DE   Human PRO852 (UNQ418) nucleotide sequence SEQ ID NO:195.
XX
KW   Human; secreted protein; transmembrane protein; PRO; EST; cytostatic;
KW   expressed sequence tag; detection; cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200053756-A2.
XX
PD   14-SEP-2000.
XX
PF   18-FEB-2000; 2000WO-US004341.
XX
PR   08-MAR-1999;   99WO-US005028.
PR   12-MAR-1999;   99US-0123957P.
PR   29-MAR-1999;   99US-0126773P.
PR   21-APR-1999;   99US-0130232P.
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PR 28-APR-1999; 99US-0131445P.
PR 14-MAY-1999; 99US-0134287P.
PR 23-JUN-1999; 99US-0141037P.
PR 26-JUL-1999; 99US-0145698P.
PR 29-OCT-1999; 99US-0162506P.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
PI Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
PI Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
PI Stewart TA, Tumas D, Williams PM, Wood WI;
XX
DR WPI; 2000-611443/58.
DR P-PSDB; AAB44270.
XX
PT Novel PRO polypeptides and polynucleotides used in detection methods, to
PT target bioactive molecules to specific cells, and to modulate cellular
PT activities.
XX
PS Claim 2; Fig 72; 636pp; English.
XX
CC AAC78458 to AAC78599 represent polynucleotide and EST (expressed sequence
CC tag) sequences which encode secreted or transmembrane PRO polypeptides.
CC The PRO polynucleotides and polypeptides have cytostatic activity. The
CC polynucleotides and polypeptides can be used for detecting the presence
CC of PRO polypeptides in samples, for linking bioactive molecules to cells
CC and for modulating biological activities of cells, using the polypeptides
CC for specific targeting. The polypeptide targeting can be used to kill the
CC target cells, e.g. for the treatment of cancers. The polypeptide pairs
CC provide specific targeting of bioactive molecules to cells. AAC78600 to
CC AAC78987 represent PCR primers and probes used in the isolation of the
CC PRO polynucleotide sequences
XX
SQ Sequence 1879 BP; 388 A; 559 C; 498 G; 434 T; 0 U; 0 Other;

Query Match 98.9%; Score 1784.4; DB 3; Length 1879;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1785; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         94 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 153

Qy         61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        154 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 213
```

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Qy      121 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      214 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 273

Qy      181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      274 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 333

Qy      241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      334 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 393

Qy      301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      394 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 453

Qy      361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      454 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 513

Qy      421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      514 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 573

Qy      481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      574 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 633

Qy      541 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      634 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 693

Qy      601 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      694 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 753

Qy      661 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      754 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 813

Qy      721 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      814 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 873

Qy      781 GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA 840
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      874 GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA 933

Qy      841 TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC 900
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      934 TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC 993

Qy      901 ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG 960
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      994 ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG 1053
```

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Qy        961 GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1054 GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC 1113

Qy       1021 CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1114 CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC 1173

Qy       1081 TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1140
              |||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||
Db       1174 TACCTGAGAGACGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1233

Qy       1141 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1234 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA 1293

Qy       1201 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1294 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC 1353

Qy       1261 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1354 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1413

Qy       1321 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1414 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1473

Qy       1381 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1474 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1533

Qy       1441 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1534 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1593

Qy       1501 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1594 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1653

Qy       1561 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1654 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1713

Qy       1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1714 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1773

Qy       1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1774 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1833

Qy       1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAA 1786
              ||||||||||||||||||||||||||||||||||||||||||||||
Db       1834 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAA 1879
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RESULT 10
AAS45960
ID AAS45960 standard; cDNA; 1879 BP.
XX
AC AAS45960;
XX
DT 18-DEC-2001 (first entry)
XX
DE Human DNA encoding PRO polypeptide sequence #36.
XX
KW PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep; ss;
KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder;
KW PCR primer.
XX
OS Homo sapiens.
XX
PN WO200168848-A2.
XX
PD 20-SEP-2001.
XX
PF 28-FEB-2001; 2001WO-US006520.
XX
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 03-MAR-2000; 2000US-0187202P.
PR 06-MAR-2000; 2000US-0186968P.
PR 14-MAR-2000; 2000US-0189320P.
PR 14-MAR-2000; 2000US-0189328P.
PR 15-MAR-2000; 2000WO-US006884.
PR 21-MAR-2000; 2000US-0190828P.
PR 21-MAR-2000; 2000US-0191007P.
PR 21-MAR-2000; 2000US-0191048P.
PR 21-MAR-2000; 2000US-0191314P.
PR 28-MAR-2000; 2000US-0192655P.
PR 29-MAR-2000; 2000US-0193032P.
PR 29-MAR-2000; 2000US-0193053P.
PR 30-MAR-2000; 2000WO-US008439.
PR 04-APR-2000; 2000US-0194449P.
PR 04-APR-2000; 2000US-0194647P.
PR 11-APR-2000; 2000US-0195975P.
PR 11-APR-2000; 2000US-0196000P.
PR 11-APR-2000; 2000US-0196187P.
PR 11-APR-2000; 2000US-0196690P.
PR 11-APR-2000; 2000US-0196820P.
PR 18-APR-2000; 2000US-0198121P.
PR 18-APR-2000; 2000US-0198585P.
PR 25-APR-2000; 2000US-0199397P.
PR 25-APR-2000; 2000US-0199550P.
PR 25-APR-2000; 2000US-0199654P.
PR 03-MAY-2000; 2000US-0201516P.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 05-JUN-2000; 2000US-0209832P.

PR 28-JUL-2000; 2000WO-US020710.
PR 22-AUG-2000; 2000US-00644848.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000WO-US034956.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI; 2001-602746/68.
DR P-PSDB; AAU29059.
XX
PT Novel nucleic acids encoding PRO polypeptides, used to diagnose the
PT presence of tumors, such as prostate and breast tumors, in mammals and to
PT screen for modulators of the compounds.
XX
PS Claim 2; Fig 71; 774pp; English.
XX
CC Sequences AAS45925-AAS46231 represent DNA molecules encoding and PCR
CC primers for PRO polypeptides of the invention. The sequences of the
CC invention can be used to detect the presence of a tumour in a mammal by
CC comparing the level of expression of a PRO polypeptide in a test sample
CC of cells from the animal and a control sample of normal cells, whereby a
CC higher level of expression in the test sample indicates the presence of a
CC tumour in the mammal. Mammals include dogs, cats, cattle, horses, sheep,
CC pigs, goats and rabbits but are preferably human. The polypeptides can be
CC used to stimulate tumour necrosis factor (TNF) alpha release from human
CC blood, when contacted with it. A specific polypeptide can be used to
CC stimulate the proliferation or differentiation of chondrocyte cells. The
CC PRO proteins can be used to determine the presence of tumours and also
CC susceptibility to tumour development, particularly adrenal, lung, colon,
CC breast, prostate, rectal, cervical, or liver tumours, in mammalian
CC subjects. The oligonucleotide probes specific for the PRO nucleic acids
CC can be used for genetic analysis of individuals with genetic disorders
XX
SQ Sequence 1879 BP; 388 A; 559 C; 498 G; 434 T; 0 U; 0 Other;

Query Match 98.9%; Score 1784.4; DB 4; Length 1879;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1785; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DT 15-APR-2003 (first entry)
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DE Human PRO polynucleotide #36.
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KW Human; PRO; gene; ss; cytostatic; tumour; cancer; breast; lung; stomach;
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PN US2003027272-A1.
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PD 06-FEB-2003.
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PF 21-JUN-2002; 2002US-00176492.
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Query Match 98.9%; Score 1784.4; DB 7; Length 1879;
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DT 07-JUL-2003 (first entry)
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XX
KW Human; secreted and transmembrane protein: PRO; gene therapy;
KW tumour necrosis factor-alpha release; TNF-alpha release;
KW chondrocyte proliferation; chondrocyte differentiation; tumour;
KW adrenal tumour; lung tumour; colon tumour; breast tumour;
KW prostate tumour; rectal tumour; cervical tumour; liver tumour; gene; ss.
XX
OS Homo sapiens.
XX
PN US2003032127-A1.
XX

PD 13-FEB-2003.
XX
PF 26-JUN-2002; 2002US-00183012.
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AC   ACA71015;
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DT   02-AUG-2003  (first entry)
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DE   Human secreted/transmembrane protein (PRO) cDNA #36.
XX
KW   Human; gene; ss; secreted and transmembrane protein; PRO; TNF-alpha;
KW   tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
KW   tissue typing.
XX
OS   Homo sapiens.
XX
PN   US2003032112-A1.
XX
PD   13-FEB-2003.
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PF   21-JUN-2002; 2002US-00176756.
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PR   18-SEP-1997;   97US-0059263P.
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Search completed: March 5, 2004, 21:23:48
Job time : 710 secs

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OM nucleic - nucleic search, using sw model

Run on: March 5, 2004, 18:32:27 ; Search time 154 Seconds
(without alignments)
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Perfect score: 1804
Sequence: 1 atgggcgcactggcccgggc.....aaaccaaaaaaaaaaaaaaa 1804

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1804	100.0	1804	4	US-09-548-372D-1	Sequence 1, Appli
2	1804	100.0	1804	4	US-09-548-367D-1	Sequence 1, Appli
3	1804	100.0	1804	4	US-09-551-853D-1	Sequence 1, Appli
4	1768.2	98.0	1873	4	US-09-215-450-18	Sequence 18, Appl
5	1765.6	97.9	1862	3	US-08-999-723-1	Sequence 1, Appli
6	1765.6	97.9	1862	3	US-09-434-427-1	Sequence 1, Appli
7	1478.6	82.0	2429	4	US-09-215-450-1	Sequence 1, Appli
8	1134.2	62.9	1545	3	US-09-717-432-1	Sequence 1, Appli
9	1134.2	62.9	1545	4	US-09-912-484-1	Sequence 1, Appli
10	1104.6	61.2	2514	4	US-09-280-116-32	Sequence 32, Appl
11	953.6	52.9	1021	4	US-09-280-116-85	Sequence 85, Appl

12	397.4	22.0	2348	4	US-09-724-566A-42	Sequence 42, Appl
13	397.4	22.0	2348	4	US-09-724-566A-44	Sequence 44, Appl
14	397.4	22.0	16080	4	US-09-724-566A-48	Sequence 48, Appl
15	395	21.9	1503	4	US-09-724-566A-1	Sequence 1, Appli
16	395	21.9	2070	4	US-09-548-372D-3	Sequence 3, Appli
17	395	21.9	2070	4	US-09-548-367D-3	Sequence 3, Appli
18	395	21.9	2070	4	US-09-551-853D-3	Sequence 3, Appli
19	395	21.9	3252	4	US-09-604-608-1	Sequence 1, Appli
20	393.4	21.8	2541	4	US-09-009-191-1	Sequence 1, Appli
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22	386	21.4	1380	4	US-09-548-372D-23	Sequence 23, Appl
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25	385	21.3	1362	4	US-09-548-372D-29	Sequence 29, Appl
26	385	21.3	1362	4	US-09-548-367D-29	Sequence 29, Appl
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28	385	21.3	1380	4	US-09-548-372D-31	Sequence 31, Appl
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34	382.4	21.2	1302	4	US-09-548-372D-25	Sequence 25, Appl
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39	381	21.1	2043	4	US-09-548-367D-7	Sequence 7, Appli
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41	380.8	21.1	1278	4	US-09-548-372D-27	Sequence 27, Appl
42	380.8	21.1	1278	4	US-09-548-367D-27	Sequence 27, Appl
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44	294	16.3	306	4	US-09-280-116-52	Sequence 52, Appl
45	291.2	16.1	1977	4	US-09-548-372D-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-09-548-372D-1
; Sequence 1, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/6280I
; CURRENT APPLICATION NUMBER: US/09/548,372D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 1804
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-548-372D-1

  Query Match   100.0%; Score 1804; DB 4; Length 1804;
  Best Local Similarity   100.0%; Pred. No. 0;
  Matches 1804; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Db       1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1680

Qy       1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740

Qy       1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAAACCAAAAAAAAAAA 1800
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAAACCAAAAAAAAAAA 1800

Qy       1801 AAAA 1804
              ||||
Db       1801 AAAA 1804
```

RESULT 2
US-09-548-367D-1
; Sequence 1, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/6280H
; CURRENT APPLICATION NUMBER: US/09/548,367D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1804
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-548-367D-1

Query Match 100.0%; Score 1804; DB 4; Length 1804;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1804; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60

Qy         61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120

Qy        121 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180

Qy        181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240

Qy        241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300

Qy        301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360

Qy        361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420

Qy        421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480

Qy        481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540

Qy        541 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600

Qy        601 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 660

Qy        661 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 720

Qy        721 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 780

Qy        781 GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA 840

Qy        841 TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC 900
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Db        841 TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC 900

Qy        901 ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG 960

Qy        961 GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC 1020

Qy       1021 CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC 1080

Qy       1081 TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1140

Qy       1141 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA 1200

Qy       1201 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC 1260

Qy       1261 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1320

Qy       1321 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1380

Qy       1381 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1440

Qy       1441 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1500

Qy       1501 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1560

Qy       1561 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1620

Qy       1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1680

Qy       1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740

Qy        1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAAACCAAAAAAAAAAA 1800
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAAACCAAAAAAAAAAA 1800

Qy        1801 AAAA 1804
               ||||
Db        1801 AAAA 1804
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RESULT 3
US-09-551-853D-1
; Sequence 1, Application US/09551853D
; Patent No. 6500667
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/6280L
; CURRENT APPLICATION NUMBER: US/09/551,853D
; CURRENT FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1804
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-551-853D-1

Query Match 100.0%; Score 1804; DB 4; Length 1804;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1804; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy           1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60

Qy          61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120

Qy         121 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180

Qy         181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240

Qy        241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300

Qy        301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360

Qy        361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420

Qy        421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480

Qy        481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540

Qy        541 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600

Qy        601 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 660

Qy        661 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 720

Qy        721 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 780

Qy        781 GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA 840

Qy        841 TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC 900

Qy        901 ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG 960

Qy        961 GAAGCTGTGGCCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GAAGCTGTGGCCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC 1020

Qy       1021 CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC 1080
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Qy       1081 TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1140

Qy       1141 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA 1200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA 1200

Qy       1201 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC 1260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC 1260

Qy       1261 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1320

Qy       1321 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1380

Qy       1381 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1440

Qy       1441 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1500

Qy       1501 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1560

Qy       1561 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1620

Qy       1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1680

Qy       1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740

Qy       1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAAACCAAAAAAAAAAA 1800
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAAACCAAAAAAAAAAA 1800

Qy       1801 AAAA 1804
              ||||
Db       1801 AAAA 1804
```

RESULT 4
US-09-215-450-18
; Sequence 18, Application US/09215450

; Patent No. 6635748
; GENERAL INFORMATION:
; APPLICANT: Giese, Klaus
; APPLICANT: Xin, Hong
; TITLE OF INVENTION: METASTATIC BREAST AND COLON CANCER REGULATED GENES
; FILE REFERENCE: 1451.100 / 210030.447
; CURRENT APPLICATION NUMBER: US/09/215,450
; CURRENT FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 18
; LENGTH: 1873
; TYPE: DNA
; ORGANISM: human
US-09-215-450-18

Query Match 98.0%; Score 1768.2; DB 4; Length 1873;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1770; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy        1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60
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Db      101 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 160

Qy       61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      161 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 220

Qy      121 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      221 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 280

Qy      181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      281 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 340

Qy      241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      341 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 400

Qy      301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      401 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 460

Qy      361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      461 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 520

Qy      421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      521 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 580

Qy      481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      581 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 640

Qy      541 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600
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Db        641 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 700

Qy        601 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 660

Db        701 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 760

Qy        661 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 720

Db        761 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 820

Qy        721 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 780

Db        821 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 880

Qy        781 GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA 840

Db        881 GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA 940

Qy        841 TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC 900

Db        941 TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC 1000

Qy        901 ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG 960

Db       1001 ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG 1060

Qy        961 GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC 1020

Db       1061 GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC 1120

Qy       1021 CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC 1080

Db       1121 CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC 1180

Qy       1081 TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1140

Db       1181 TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1240

Qy       1141 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA 1200

Db       1241 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA 1300

Qy       1201 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC 1260

Db       1301 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC 1360

Qy       1261 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1320

Db       1361 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1420

Qy       1321 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1380

Db       1421 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1480

Qy       1381 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1440
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Db        1481 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1540

Qy        1441 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1500
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1541 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1600

Qy        1501 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1560
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1601 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1660

Qy        1561 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1620
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1661 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1720

Qy        1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1680
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1721 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1780

Qy        1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1781 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1840

Qy        1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAA 1773
               |||||||||||||||||| ||  ||||||||
Db        1841 CTCCCTACTTCCAAGAAAAAAAAAAAAAAAAA 1873


RESULT 5
US-08-999-723-1
; Sequence 1, Application US/08999723A
; Patent No. 6025180
; GENERAL INFORMATION:
;  APPLICANT: Powell, David J.
;  APPLICANT: Southan, Christopher
;  APPLICANT: Chapman, Conrad G.
;  APPLICANT: Evans, Joanne R.
;  TITLE OF INVENTION: ASP1
;  FILE REFERENCE: GH70262
;  CURRENT APPLICATION NUMBER: US/08/999,723A
;  CURRENT FILING DATE: 1997-10-06
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 1862
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-08-999-723-1

  Query Match             97.9%;  Score 1765.6;  DB 3;  Length 1862;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 1768;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy           1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          91 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 150

Qy          61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120
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Db        151 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 210

Qy        121 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180

Db        211 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 270

Qy        181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240

Db        271 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 330

Qy        241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300

Db        331 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 390

Qy        301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360

Db        391 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 450

Qy        361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420

Db        451 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 510

Qy        421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480

Db        511 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 570

Qy        481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540

Db        571 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 630

Qy        541 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600

Db        631 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 690

Qy        601 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 660

Db        691 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 750

Qy        661 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 720

Db        751 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 810

Qy        721 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 780

Db        811 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 870

Qy        781 GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA 840

Db        871 GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA 930

Qy        841 TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC 900

Db        931 TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC 990

Qy        901 ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG 960
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Db        991 ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG 1050

Qy        961 GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1051 GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC 1110

Qy       1021 CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1111 CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC 1170

Qy       1081 TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1140
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db       1171 TACCTGAGAGACGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1230

Qy       1141 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1231 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA 1290

Qy       1201 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1291 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC 1350

Qy       1261 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1351 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1410

Qy       1321 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1411 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1470

Qy       1381 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1471 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1530

Qy       1441 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1531 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1590

Qy       1501 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1591 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1650

Qy       1561 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1651 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1710

Qy       1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1711 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1770

Qy       1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1771 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1830

Qy       1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAA 1772
              |||||||||||||||||||  ||  |||||||
Db       1831 CTCCCTACTTCCAAGAAAAAAAAAAAAAAAA 1862
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RESULT 6
US-09-434-427-1
; Sequence 1, Application US/09434427
; Patent No. 6162630
; GENERAL INFORMATION:
; APPLICANT: POWELL, DAVID J.
; APPLICANT: SOUTHAN, CHRISTOPHER
; APPLICANT: CHAPMAN, CONRAD G.
; APPLICANT: EVANS, JOANNE R.
; TITLE OF INVENTION: ASP1
; FILE REFERENCE: GH-70262-D1
; CURRENT APPLICATION NUMBER: US/09/434,427
; CURRENT FILING DATE: 1999-11-04
; EARLIER APPLICATION NUMBER: US 08/999,723
; EARLIER FILING DATE: 1997-10-06
; EARLIER APPLICATION NUMBER: UK 9626022.9
; EARLIER FILING DATE: 1996-12-14
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1862
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
US-09-434-427-1

  Query Match 97.9%; Score 1765.6; DB 3; Length 1862;
  Best Local Similarity 99.8%; Pred. No. 0;
  Matches 1768; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy          1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         91 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 150

Qy         61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        151 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 210

Qy        121 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        211 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 270

Qy        181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        271 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 330

Qy        241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        331 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 390

Qy        301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        391 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 450

Qy        361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        451 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 510

Qy        421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        511 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 570

Qy        481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        571 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 630

Qy        541 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        631 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 690

Qy        601 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        691 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 750

Qy        661 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        751 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 810

Qy        721 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        811 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 870

Qy        781 GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        871 GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA 930

Qy        841 TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        931 TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC 990

Qy        901 ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        991 ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG 1050

Qy        961 GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1051 GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC 1110

Qy       1021 CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1111 CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC 1170

Qy       1081 TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1140
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db       1171 TACCTGAGAGACGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1230

Qy       1141 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1231 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA 1290

Qy       1201 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1291 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC 1350
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Qy       1261 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1351 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1410

Qy       1321 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1411 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1470

Qy       1381 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1471 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1530

Qy       1441 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1531 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1590

Qy       1501 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1591 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1650

Qy       1561 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1651 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1710

Qy       1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1711 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1770

Qy       1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1771 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1830

Qy       1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAA 1772
             |||||||||||||||||| ||  |||||||
Db       1831 CTCCCTACTTCCAAGAAAAAAAAAAAAAAAA 1862
```

RESULT 7
US-09-215-450-1
; Sequence 1, Application US/09215450
; Patent No. 6635748
; GENERAL INFORMATION:
; APPLICANT: Giese, Klaus
; APPLICANT: Xin, Hong
; TITLE OF INVENTION: METASTATIC BREAST AND COLON CANCER REGULATED GENES
; FILE REFERENCE: 1451.100 / 210030.447
; CURRENT APPLICATION NUMBER: US/09/215,450
; CURRENT FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 2429
; TYPE: DNA
; ORGANISM: human
US-09-215-450-1

Query Match 82.0%; Score 1478.6; DB 4; Length 2429;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 1484; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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Qy        305 CGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGAACCC 364
              | ||  |||||||||||||||||||||||||||||||||||||||||||||||| | |||||
Db        213 CTCACCAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGCAGGAAACCC 272

Qy        365 CGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCCAAGG 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        273 CGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCCAAGG 332

Qy        425 GCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAAGACC 484
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        333 GCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAAGACC 392

Qy        485 TCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATTTTTG 544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        393 TCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATTTTTG 452

Qy        545 AATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCTTATG 604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        453 AATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCTTATG 512

Qy        605 CCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACACAAG 664
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        513 CCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACACAAG 572

Qy        665 CAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCTGGAT 724
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        573 CAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCTGGAT 632

Qy        725 CTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAAGGAG 784
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        633 CTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAAGGAG 692

Qy        785 ACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAATTGG 844
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        693 ACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAATTGG 752

Qy        845 AAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCCATCG 904
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        753 AAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCCATCG 812

Qy        905 TGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTGGAAG 964
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        813 TGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTGGAAG 872

Qy        965 CTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCCCAGC 1024
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        873 CTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCCCAGC 932

Qy       1025 TGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATCTACC 1084
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        933 TGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATCTACC 992

Qy       1085 TGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTACATTC 1144
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                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          993 TGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTACATTC 1052

Qy         1145 AGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCATCCA 1204
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1053 AGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCATCCA 1112

Qy         1205 CAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGACAGAG 1264
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1113 CAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGACAGAG 1172

Qy         1265 CCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCAGTGT 1324
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1173 CCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCAGTGT 1232

Qy         1325 CTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCTCAGT 1384
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1233 CTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCTCAGT 1292

Qy         1385 CTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGAGCCA 1444
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1293 CTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGAGCCA 1352

Qy         1445 TCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCCCGTG 1504
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1353 TCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCCCGTG 1412

Qy         1505 ACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATAGCCA 1564
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1413 ACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATAGCCA 1472

Qy         1565 GGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGCAGCA 1624
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1473 GGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGCAGCA 1532

Qy         1625 GCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCTGCTC 1684
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1533 GCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCTGCTC 1592

Qy         1685 CCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATCCTCC 1744
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1593 CCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATCCTCC 1652

Qy         1745 CTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAAACCAAAAAAAA 1797
                ||||||||||||||||||||||||||||||||||||||||||||||||| | |
Db         1653 CTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAAACCAAAACAGA 1705
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RESULT 8
US-09-717-432-1
; Sequence 1, Application US/09717432
; Patent No. 6291223
; GENERAL INFORMATION:
; APPLICANT: ZHU, YUAN
; APPLICANT: LI, XIAOTONG
; APPLICANT: CHRISTIE, GARY
; APPLICANT: POWELL, DAVID J.

; TITLE OF INVENTION: Mouse Aspartic Secretase-1 (mASP1)
; FILE REFERENCE: GP-70663
; CURRENT APPLICATION NUMBER: US/09/717,432
; CURRENT FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: 60/166,974
; PRIOR FILING DATE: 1999-11-23
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
;   LENGTH: 1545
;   TYPE: DNA
;   ORGANISM: MUS MUSCULUS
US-09-717-432-1

  Query Match 62.9%; Score 1134.2; DB 3; Length 1545;
  Best Local Similarity 83.6%; Pred. No. 5.5e-260;
  Matches 1302; Conservative 0; Mismatches 243; Indels 12; Gaps 1;

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Qy          1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60
              ||||||| |||   || || ||  |||| |   ||||||| ||||||||| || | ||
Db          1 ATGGGCGCGCTGCTTCGAGCACTCTTGCTCCTGGTGCTGGCGCAGTGGCTCTTGAGTGCG 60

Qy         61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120
              | ||| | ||||||||||||||||||||||||||||||  ||||||| ||||||||||
Db         61 GTCCCCGCGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCAAGTGGCCGGGGCCACGAAC 120

Qy        121 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180
              | |  ||   || |    || |||| |||||||| |    || ||  ||||| ||  ||
Db        121 CACAGAGCCTCGGCTGTTCCCGGACTCGGGACCCCCGAGTTGCCCCGGGCCGATGGTCTG 180

Qy        181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240
              || ||||| |||||||||| |  |||               | |||||||||||||| |||
Db        181 GCCCTCGCACTGGAGCCTGTCAGGGC----------TACTGCCAACTTCTTGGCTATG 228

Qy        241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300
              || |||||||| ||||||||||||||||||||||||||| ||||||||||||||||||
Db        229 GTGGACAACCTTCAGGGGGACTCTGGCCGCGGCTACTACCTAGAGATGCTGATCGGGACC 288

Qy        301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360
              || ||||||||| |||||||||| || |||||||||||||||||| || ||||||||
Db        289 CCTCCGCAGAAGGTACAGATTCTTGTGGACACTGGAAGCAGTAACTTCGCTGTGGCAGGT 348

Qy        361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420
               |||| |||||||||||||||| |||||||| ||||||| || |||||||||| ||||
Db        349 GCCCCACACTCCTACATAGACACCTACTTTGACTCAGAGAGCTCCAGCACATACCACTCC 408

Qy        421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480
              |||||||||| ||||| |||||||||||||| |||||||||| ||||| ||||| ||
Db        409 AAGGGCTTTGATGTCACTGTGAAGTACACACAGGGAAGCTGGACTGGCTTTGTTGGTGAG 468

Qy        481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540
              ||||| |||||||||| |||||||||| |  |||||  | ||||| ||||||||||||
Db        469 GACCTTGTCACCATCCCAAAAGGCTTCAACAGCTCTTTCTTGGTCAATATTGCCACTATT 528

Qy        541 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600
              || || || |||||||||||||||||||| |||||||||||||||| ||||| || |||
Db        529 TTCGAGTCTGAGAATTTCTTTTTGCCTGGTATTAAATGGAATGGAATCCTTGGACTTGCT 588
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Qy        601 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 660
              |||||  |  | |||||||||||||| |||||||||| || || || ||||||||| |
Db        589 TATGCTGCTTTGGCCAAGCCATCAAGCTCTCTGGAGACATTTTTTGATTCCCTGGTGGCC 648

Qy        661 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 720
              |||||||| || ||  || ||||||||||||||||||| || || || ||||| || |||
Db        649 CAAGCAAAGATTCCAGACATTTTCTCCATGCAGATGTGCGGGGCTGGATTGCCAGTAGCT 708

Qy        721 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 780
              || ||||| ||||||||||||||||||||| ||||||| ||||||||||||||||||||
Db        709 GGTTCTGGTACCAACGGAGGTAGTCTTGTCCTGGGTGGGATTGAACCAAGTTTGTATAAA 768

Qy        781 GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA 840
              ||||| |||||||||||||| ||||| || || |||||||| || |||||||| |||||
Db        769 GGAGATATCTGGTATACCCCAATTAAAGAGGAATGGTACTATCAAATAGAAATCCTGAAG 828

Qy        841 TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC 900
              |||||||||||||||| | ||| || ||||||||||||||||||||||||||||||||
Db        829 TTGGAAATTGGAGGCCAGAACCTCAACCTGGACTGCAGAGAGTATAACGCAGACAAGGCC 888

Qy        901 ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG 960
              || |||||||||||||||||| ||||||||||||||||||||||||||| ||||||
Db        889 ATTGTGGACAGTGGCACCACGCTCCTGCGCCTGCCCCAGAAGGTGTTTGATGCAGTGGTG 948

Qy        961 GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC 1020
              |||||||||| ||  |||||||||||||| || |||||||| |||||||| ||| ||
Db        949 GAAGCTGTGGCACGAACATCTCTGATTCCAGAGTTTTCTGATGGCTTCTGGACAGGGGCC 1008

Qy       1021 CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC 1080
              |||||||| |||||||| ||||| ||||| || ||| | || |||||||| || || |||
Db        1009 CAGCTGGCATGCTGGACAAATTCTGAAACGCCATGGGCATATTTCCCTAAGATTTCTATC 1068

Qy       1081 TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1140
              ||||||||||||||||  ||||  | || ||||| ||||| || || || ||||| |||
Db        1069 TACCTGAGAGATGAGAATGCCAGTCGCTCCTTCCGGATCACCATTCTCCCACAGCTCTAC 1128

Qy       1141 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA 1200
              |||||||||||||||| || ||  | |||||||||| ||||| || || || ||| |
Db        1129 ATTCAGCCCATGATGGGAGCTGGTTTCAATTATGAATGCTACCGTTTTGGTATCTCCTCT 1188

Qy       1201 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC 1260
              |||||||||||||||||| ||||| || |||||||| |||||||||| |||| |||
Db        1189 TCCACAAATGCGCTGGTGATTGGTGCGACCGTGATGGAAGGCTTCTACGTGGTCTTTGAC 1248

Qy       1261 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1320
              ||||| |||| |||||||||||| |||| ||| |||||||||| |||| |||| |  ||
Db        1249 AGAGCTCAGAGGAGGGTGGGCTTTGCAGTGAGTCCCTGTGCAGAGATTGAAGGTACCACA 1308

Qy       1321 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1380
              |||||||||||||| ||||| || || || || ||  |||||||||||||||| || ||
Db        1309 GTGTCTGAAATTTCTGGGCCCTTTTCCACGGAAGACATAGCCAGCAACTGTGTTCCAGCA 1368

Qy       1381 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1440
              ||| || |||  |||||||| |||||||||||||||||| || ||||| || ||||||
Db        1369 CAGGCTCTGAATGAGCCCATCTTGTGGATTGTGTCCTATGCCCTGATGAGTGTGTGTGGA 1428
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Qy       1441 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1500
             ||||| ||||| ||  | ||| |||| |||||||| ||| | |  || |  | |  ||||
Db       1429 GCCATTCTCCTGGTTCTGATCCTCCTCCTGCTGCTCCCGCTGCACTGCCGTCATGCCCCC 1488

Qy       1501 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGA 1557
             || |||||||||| || || |||||||||| || ||||||||||||||||||||
Db       1489 CGAGACCCTGAGGTAGTTAACGATGAGTCCTCACTAGTCAGACATCGCTGGAAATGA 1545
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RESULT 9
US-09-912-484-1
; Sequence 1, Application US/09912484
; Patent No. 6358725
; GENERAL INFORMATION:
; APPLICANT: Christie, Gary
; APPLICANT: Li, Xiaotong
; APPLICANT: Powell, David J.
; APPLICANT: Zhu, Yuan
; TITLE OF INVENTION: Mouse Aspartic Secretase-1 (mASP1)
; FILE REFERENCE: GP-70663-D1
; CURRENT APPLICATION NUMBER: US/09/912,484
; CURRENT FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 60/166,974
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: 09/717,432
; PRIOR FILING DATE: 2000-11-21
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1545
; TYPE: DNA
; ORGANISM: MUS MUSCULUS
US-09-912-484-1

Query Match 62.9%; Score 1134.2; DB 4; Length 1545;
Best Local Similarity 83.6%; Pred. No. 5.5e-260;
Matches 1302; Conservative 0; Mismatches 243; Indels 12; Gaps 1;

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Qy          1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60
              |||||||| |||   || || ||  |||| |   ||||||| ||||||||| || | ||
Db          1 ATGGGCGCGCTGCTTCGAGCACTCTTGCTCCTGGTGCTGGCGCAGTGGCTCTTGAGTGCG 60

Qy         61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120
              | ||| | ||||||||||||||||||||||||||||||||  ||||||| ||||||||||
Db         61 GTCCCCGCGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCAAGTGGCCGGGGCCACGAAC 120

Qy        121 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180
              | |  ||   || |    || |||| ||||||||| |    || ||  ||||| ||  ||
Db        121 CACAGAGCCTCGGCTGTTCCCGGACTCGGGACCCCCGAGTTGCCCCGGGCCGATGGTCTG 180

Qy        181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240
              || ||||| |||||||||| |  |||               | ||||||||||||| |||
Db        181 GCCCTCGCACTGGAGCCTGTCAGGGC-----------TACTGCCAACTTCTTGGCTATG 228

Qy        241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300
              || |||||||| ||||||||||||||||||||||||||| ||||||||||||||||||
Db        229 GTGGACAACCTTCAGGGGGACTCTGGCCGCGGCTACTACCTAGAGATGCTGATCGGGACC 288
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Qy        301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360
              ||  |||||||||  ||||||||||  ||  ||||||||||||||||||||  ||  ||||||||
Db        289 CCTCCGCAGAAGGTACAGATTCTTGTGGACACTGGAAGCAGTAACTTCGCTGTGGCAGGT 348

Qy        361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420
               ||||  ||||||||||||||||||  ||||||||  |||||||  ||  ||||||||||  ||||
Db        349 GCCCCACACTCCTACATAGACACCTACTTTGACTCAGAGAGCTCCAGCACATACCACTCC 408

Qy        421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480
              ||||||||||  |||||  ||||||||||||||  ||||||||||  |||||  |||||  ||
Db        409 AAGGGCTTTGATGTCACTGTGAAGTACACACAGGGAAGCTGGACTGGCTTTGTTGGTGAG 468

Qy        481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540
              |||||  ||||||||||  ||||||||||  |  |||||  |  |||||  ||||||||||||
Db        469 GACCTTGTCACCATCCCAAAAGGCTTCAACAGCTCTTTCTTGGTCAATATTGCCACTATT 528

Qy        541 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600
              ||  ||  ||  ||||||||||||||||||||  ||||||||||||||||||  |||||  ||  |||
Db        529 TTCGAGTCTGAGAATTTCTTTTTGCCTGGTATTAAATGGAATGGAATCCTTGGACTTGCT 588

Qy        601 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 660
              |||||  |  |  ||||||||||||||  ||||||||||  ||  ||  ||  |||||||||  |
Db        589 TATGCTGCTTTGGCCAAGCCATCAAGCTCTCTGGAGACATTTTTTGATTCCCTGGTGGCC 648

Qy        661 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 720
              ||||||||  ||  ||  ||  ||||||||||||||||||  ||  ||  ||  |||||  ||  |||
Db        649 CAAGCAAAGATTCCAGACATTTTCTCCATGCAGATGTGCGGGGCTGGATTGCCAGTAGCT 708

Qy        721 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 780
              ||  |||||  ||||||||||||||||||||  |||||||  ||||||||||||||||||||
Db        709 GGTTCTGGTACCAACGGAGGTAGTCTTGTCCTGGGTGGGATTGAACCAAGTTTGTATAAA 768

Qy        781 GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA 840
              |||||  ||||||||||||||  |||||  ||  ||  ||||||||  ||  ||||||||  |||||
Db        769 GGAGATATCTGGTATACCCCAATTAAAGAGGAATGGTACTATCAAATAGAAATCCTGAAG 828

Qy        841 TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC 900
              ||||||||||||||||  |  |||  ||  ||||||||||||||||||||||||||||||
Db        829 TTGGAAATTGGAGGCCAGAACCTCAACCTGGACTGCAGAGAGTATAACGCAGACAAGGCC 888

Qy        901 ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG 960
              ||  ||||||||||||||||||  ||||||||||||||||||||||||||||||  ||||||
Db        889 ATTGTGGACAGTGGCACCACGCTCCTGCGCCTGCCCCAGAAGGTGTTTGATGCAGTGGTG 948

Qy        961 GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC 1020
              ||||||||||  ||  ||||||||||||||||  ||  ||||||||  ||||||||  |||  ||
Db        949 GAAGCTGTGGCACGAACATCTCTGATTCCAGAGTTTTCTGATGGCTTCTGGACAGGGGCC 1008

Qy       1021 CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC 1080
              ||||||||  ||||||||  |||||  |||||  ||  |||  |  ||  ||||||||  ||  ||  |||
Db       1009 CAGCTGGCATGCTGGACAAATTCTGAAACGCCATGGGCATATTTCCCTAAGATTTCTATC 1068

Qy       1081 TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1140
              ||||||||||||||||||  ||||  |  ||  |||||  |||||  ||  ||  ||  |||||  |||
Db       1069 TACCTGAGAGATGAGAATGCCAGTCGCTCCTTCCGGATCACCATTCTCCCACAGCTCTAC 1128
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Qy       1141 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA 1200
             ||||||||||||||||| || ||  | |||||||||| ||||| || || || ||| |
Db       1129 ATTCAGCCCATGATGGGAGCTGGTTTCAATTATGAATGCTACCGTTTTGGTATCTCCTCT 1188

Qy       1201 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC 1260
             |||||||||||||||||||| ||||| || |||||||| |||||||||| |||| |||
Db       1189 TCCACAAATGCGCTGGTGATTGGTGCGACCGTGATGGAAGGCTTCTACGTGGTCTTTGAC 1248

Qy       1261 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1320
             ||||| |||| |||||||||||| |||| ||| |||||||||| |||| |||| |  ||
Db       1249 AGAGCTCAGAGGAGGGTGGGCTTTGCAGTGAGTCCCTGTGCAGAGATTGAAGGTACCACA 1308

Qy       1321 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1380
             |||||||||||||| ||||| || || || || ||  |||||||||||||||| || ||
Db       1309 GTGTCTGAAATTTCTGGGCCCTTTTCCACGGAAGACATAGCCAGCAACTGTGTTCCAGCA 1368

Qy       1381 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1440
             ||| || |||  |||||||| |||||||||||||||||||| || ||||| || ||||||
Db       1369 CAGGCTCTGAATGAGCCCATCTTGTGGATTGTGTCCTATGCCCTGATGAGTGTGTGTGGA 1428

Qy       1441 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1500
             ||||| ||||| ||  | ||| |||| |||||||| ||| | |  || |  | |  ||||
Db       1429 GCCATTCTCCTGGTTCTGATCCTCCTCCTGCTGCTCCCGCTGCACTGCCGTCATGCCCCC 1488

Qy       1501 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGA 1557
             || |||||||||| || || |||||||||| || ||||||||||||||||||||
Db       1489 CGAGACCCTGAGGTAGTTAACGATGAGTCCTCACTAGTCAGACATCGCTGGAAATGA 1545
```

RESULT 10
US-09-280-116-32
; Sequence 32, Application US/09280116A
; Patent No. 6331427
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs
; FILE REFERENCE: 5800-24, 035800/176965
; CURRENT APPLICATION NUMBER: US/09/280,116A
; CURRENT FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 268
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32
;   LENGTH: 2514
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: aspartyl proteases
US-09-280-116-32

  Query Match   61.2%; Score 1104.6; DB 4; Length 2514;
  Best Local Similarity   92.9%; Pred. No. 7.1e-253;
  Matches 1428; Conservative   0; Mismatches   64; Indels   45; Gaps   24;

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Qy        305 CGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGAACCC 364
              | ||  ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db        213 CTCACCAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGG-AGGAACCC 271
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Qy        365 CGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCCAAGG 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        272 CGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCCAAGG 331

Qy        425 GCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAAGACC 484
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        332 GCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAAGACC 391

Qy        485 TCGTCACCATCCCCAAAGGCTTC-AATACTTCTTTTCTTGTCAACATTGCCACTATTTTT 543
              |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db        392 TCGTCACCATCCCCAAAGGCTTCAAATACTTCTTTTCTTGTCAACATTGCCACTATTTTT 451

Qy        544 GAATCAGA-GAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCTTA 602
              |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        452 GAATCAGAGGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCTTA 511

Qy        603 TGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTG---AC 659
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||   ||
Db        512 TGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGAACAC 571

Qy        660 ACAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCC-GGCTTGCCCGTTG 718
              |     ||    ||| ||||||||||||||||||||||||||| |||||||||||||
Db        572 AAGCAAAACATCCCCAAACGTTTTCTCCATGCAGATGTGTGGAGCCGGGCTTGCCCGTTG 631

Qy        719 CTGG-----ATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTT 773
                |       |  || ||||||||||||||||||||||||||||||||||||||||||
Db        632 GCTGGGATTCTGGGGAACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTT 691

Qy        774 GTATAAAGGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAAT 833
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        692 GTATAAAGGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAAT 751

Qy        834 TCTGAAATT---GGAAATTGGAGGCCAAAGCCTTAAT------CTGGACTGCAGAGAGTA 884
              |||   ||  |   | ||  | ||||||||||| |||||           | |  ||
Db        752 TCTTGAAATTGGGAAATTGGGAGGCCAAAGCTTTAATTCTTGGGACTGCAGGAGGAGTAT 811

Qy        885 TAACGCAGACAAGG--CCATCGTGGACAGT-GGCACCACGCTGCTGCGCCT--GCCCCAG 939
              |||||||||||||   |     |||||||| ||||||||||||||||||    ||||||
Db        812 TAACGCAGACAAGGGCCATCGTTGGACAGTGGGCACCACGCTGCTGCGCCTTGCCCCCAG 871

Qy        940 AAGGTGTTTGATGCGGTGGT-GGAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTC 998
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        872 AAGGTGTTTGATGCGGTGGTGGGAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTC 931

Qy        999 TGATGGTTTCTGGACTGGGTCCCAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTC 1058
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        932 TGATGGTTTCTGGACTGGGTCCCAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTC 991

Qy       1059 TTACTTCCCTAAAATCTCCATCTACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTAT 1118
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        992 TTACTTCCCTAAAATCTCCATCTACCTGAGAGACGAGAACTCCAGCAGGTCATTCCGTAT 1051

Qy       1119 CACAATCCTGCCTCAGCTTTACATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATG 1178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1052 CACAATCCTGCCTCAGCTTTACATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATG 1111

Qy       1179 TTACCGATTCGGCATTTCCCCATCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGA 1238
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                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1112 TTACCGATTCGGCATTTCCCCATCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGA 1171

Qy         1239 GGGCTTCTACGTCATCTTCGACAGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTG 1298
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1172 GGGCTTCTACGTCATCTTCGACAGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTG 1231

Qy         1299 TGCAGAAATTGCA-GGTGCTGC-AGTGTCTGAAATTTCCGGGCCTTTCTC-AACAGAGGA 1355
                ||||||||||||| |||||||| ||||||||||||||||||||||||||| |||||||||
Db         1232 TGCAGAAATTGCACGGTGCTGCAAGTGTCTGAAATTTCCGGGCCTTTCTCAAACAGAGGA 1291

Qy         1356 TGTAGCCAG-CAACTGTGTCCCCGCTC-AGTCTTTGAGCGA-GCCCATTTTGTGGATTGT 1412
                ||||||||| ||||||||||||||||| ||||||||||||| ||||||||||||||||||
Db         1292 TGTAGCCAGCCAACTGTGTCCCCGCTCAAGTCTTTGAGCGACGCCCATTTTGTGGATTGT 1351

Qy         1413 GTCC----TATGCGCTCATGAGCGTCTGTGG-AGCCATCCTCCTTGTC-TTAATCGTCCT 1466
                ||||       || |     ||||||||||| |||||||||||||||| |||||
Db         1352 GTCCCTATGCCGCTCAATGAAGCGTCTGTGGAAGCCATCCTCCTTGTCGTTAATTCAGTC 1411

Qy         1467 GCTGCTGC----TGCCGTTCCGGTGTCAGCGTCGCCCCCGTGACCCTGAGGTCGTCAATG 1522
                ||||||||    ||||||||||||||||||||||||||||||||||||||||||||||||
Db         1412 GCTGCTGCTGCTTGCCGTTCCGGTGTCAGCGTCGCCCCCGTGACCCTGAGGTCGTCAATG 1471

Qy         1523 ATGAGTCCTCTCT-GGTCAGACATCGCTGGAAATGAATAGCCAGGCCTGACCTCAAGCAA 1581
                ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db         1472 ATGAGTCCTCTCTGGGTCAGACATCGCTGGAAATGAATAGCCAGGCCTGACCTCAAGCAA 1531

Qy         1582 CCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGCAGCAGCCGGGATCGATGGTGG 1641
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1532 CCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGCAGCAGCCGGGATCGATGGTGG 1591

Qy         1642 CGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCTGCTCCCAGATGCCTTCTAGAT 1701
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1592 CGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCTGCTCCCAGATGCCTTCTAGAT 1651

Qy         1702 TCACTGTCTTTTGATTCTTGATTTTCAAGC-TTTCAAATCCTCCCTACTTCCAAGAAAAA 1760
                |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db         1652 TCACTGTCTTTTGATTCTTGATTTTCAAGCTTTTCAAATCCTCCCTACTTCCAAGAAAAA 1711

Qy         1761 TAATTAAAAAAAAAACTTCATTCTAAACCAAAAAAAA 1797
                ||||||||||||||||||||||||||||||||| | |
Db         1712 TAATTAAAAAAAAAACTTCATTCTAAACCAAAACAGA 1748
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RESULT 11
US-09-280-116-85
; Sequence 85, Application US/09280116A
; Patent No. 6331427
; GENERAL INFORMATION:
;  APPLICANT: Robison, Keith E.
;  TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs
;  FILE REFERENCE: 5800-24, 035800/176965
;  CURRENT APPLICATION NUMBER: US/09/280,116A
;  CURRENT FILING DATE: 1999-03-26
;  NUMBER OF SEQ ID NOS: 268
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 85
```

; LENGTH: 1021
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: aspartyl proteases
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1021)
; OTHER INFORMATION: n = a, t, c or g
US-09-280-116-85

Query Match 52.9%; Score 953.6; DB 4; Length 1021;
Best Local Similarity 98.8%; Pred. No. 3.7e-217;
Matches 971; Conservative 0; Mismatches 10; Indels 2; Gaps 1;

```
Qy          98 TCCGGGTGGCCGCGGCCACGAACCGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTG 157
               ||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db          38 TCCGGGTGGCCGCGGCCACGAACCGCGTAGTTGCGCCCACCCCGGGACCCGGGAGCCCTG 97

Qy         158 CCGAGCGCCACGCCGACGGCTTGGCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGG 217
               |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db          98 CCGAGCGCCACGCCGACGGCTNGGCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGG 157

Qy         218 GCGCCGCCAACTTCTTGGCCATGGTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACT 277
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         158 GCGCCGCCAACTTCTTGGCCATGGTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACT 217

Qy         278 ACCTGGAGATGCTGATCGGGACCCCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAA 337
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         218 ACCTGGAGATGCTGATCGGGACCCCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAA 277

Qy         338 GCAGTAACTTTGCCGTGGCAGGAACCCCGCACTCCTACATAGACACGTACTTTGACACAG 397
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         278 GCAGTAACTTTGCCGTGGCAGGAACCCCGCACTCCTACATAGACACGTACTTTGACACAG 337

Qy         398 AGAGGTCTAGCACATACCGCTCCAAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAA 457
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         338 AGAGGTCTAGCACATACCGCTCCAAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAA 397

Qy         458 GCTGGACGGGCTTCGTTGGGGAAGACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTT 517
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         398 GCTGGACGGGCTTCGTTGGGGAAGACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTT 457

Qy         518 TTCTTGTCAACATTGCCACTATTTTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAAT 577
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         458 TTCTTGTCAACATTGCCACTATTTTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAAT 517

Qy         578 GGAATGGAATACTTGGCCTAGCTTATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGA 637
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         518 GGAATGGAATACTTGGCCTAGCTTATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGA 577

Qy         638 CCTTCTTCGACTCCCTGGTGACACAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGT 697
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         578 CCTTCTTCGACTCCCTGGTGACACAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGT 637

Qy         698 GTGGAGCCGGCTTGCCCGTTGCTGGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTG 757
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        638 GTGGAGCCGGCTTGCCCGTTGCTGGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTG 697

Qy        758 GAATTGAACCAAGTTTGTATAAAGGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGT 817
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        698 GAATTGAACCAAGTTTGTATAAAGGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGT 757

Qy        818 ACTACCAGATAGAAATTCTGAAATTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCA 877
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        758 ACTACCAGATAGAAATTCTGAAATTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCA 817

Qy        878 GAGAGTATAACGCAGACAAGGCCATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCC 937
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        818 GAGAGTATAACGCAGACAAGGCCATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCC 877

Qy        938 AGAAGGTGTTTGATGC--GGTGGTGGAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATT 995
              ||||||||||||||||  |  |  | ||||||||||||||||||||||||||||||||||
Db        878 AGAAGGTGTTTGATGCCGGTGGTGGAAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATT 937

Qy        996 CTCTGATGGTTTCTGGACTGGGTCCCAGCTGGCGTGCTGGACGAATTCGGAAACACCTTG 1055
              ||||||||||||||||||||||||  ||||||||||||||||||||||||||||||||||
Db        938 CTCTGATGGTTTCTGGACTGGGTCCCACTTGGCGTGCTGGACGAATTCGGAAACACCTTG 997

Qy       1056 GTCTTACTTCCCTAAAATCTCCA 1078
              |||||||||||||||||||  ||
Db        998 GTCTTACTTCCCTAAAATCTTCA 1020
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RESULT 12
US-09-724-566A-42
; Sequence 42, Application US/09724566A
; Patent No. 6627739
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Guriqbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, No. 6627739mand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; TITLE OF INVENTION: Methods
; FILE REFERENCE: 228-US-NEWC2
; CURRENT APPLICATION NUMBER: US/09/724,566A
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 42

; LENGTH: 2348
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-566A-42

Query Match 22.0%; Score 397.4; DB 4; Length 2348;
Best Local Similarity 55.0%; Pred. No. 7.1e-85;
Matches 863; Conservative 0; Mismatches 676; Indels 30; Gaps 3;

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Qy          2 TGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCCG 61
              |||| |||   ||| |||     |    |||  |||  |||||| ||  ||   |  | |
Db        238 TGGGGGCAGGCGCCAGGGACGGACGTGGGCCAGTGCGAGCCCAGAGGGCCCGAAGGCCGG 297

Qy         62 CCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAACC 121
               ||     ||||||  || |    |  ||| |  ||  || ||| |||||    |   |
Db        298 GGCCCACCATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGC 357

Qy        122 GCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTGG 181
              |     |  ||   | ||   | ||   ||         ||  |   |  |||
Db        358 CTGCCCACGGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCC 417

Qy        182 CGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGC---------------- 224
              | || |  |||  ||   ||| || | ||  ||  |   |||
Db        418 CCCTGGGGCTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGG 477

Qy        225 -CAACTTCTTGGCCATGGTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGG 283
               || |||  |||  ||||| |||||||||  |||  | || || |  |||||||||  |||
Db        478 GCAGCTTTGTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGG 537

Qy        284 AGATGCTGATCGGGACCCCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTA 343
              |||||    | || | ||||||||||| |||  | || || || || || || |||||||
Db        538 AGATGACCGTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTA 597

Qy        344 ACTTTGCCGTGGCAGGAACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGT 403
              ||||||| ||||  |   |||| ||| ||| | |  |    ||||   | |   ||  ||
Db        598 ACTTTGCAGTGGGTGCTGCCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGT 657

Qy        404 CTAGCACATACCGCTCCAAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGA 463
              | ||||||||||  |   |   |  ||   |||  ||||| || || |  |||
Db        658 CCAGCACATACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGG 717

Qy        464 CGGGCTTCGTTGGGGAAGACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTG 523
              ||     | ||    ||||| || | ||||||| | |||  |||     || | | ||
Db        718 AAGGGGAGCTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTG 777

Qy        524 TCAACATTGCCACTATTTTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATG 583
              |||||||||  | ||   |||||||||| || |||||  |    ||    || ||| | |
Db        778 CCAACATTGCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAG 837

Qy        584 GAATACTTGGCCTAGCTTATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCT 643
              | ||  ||  ||  ||  ||  |||||      ||||||  |||        ||  |||||| | ||||
Db        838 GCATCCTGGGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCT 897

Qy        644 TCGACTCCCTGGTGACACAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAG 703
              | |||||  |||||  |   ||   |   ||  | ||||||  | ||||||  |||||  | |||||  |
Db        898 TTGACTCTCTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCAGCTTTGTGGTG 957
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```
Qy        704 CCGGCTTGCCCGT----------TGCTGGATCTGGGACCAACGGAGGTAGTCTTGTCTTGG 754
              | ||||| ||| |          ||  |     |   |   |||||| ||  |  || | |
Db        958 CTGGCTTCCCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGGAGCATGATCATTG 1017

Qy        755 GTGGAATTGAACCAAGTTTGTATAAAGGAGACATCTGGTATACCCCTATTAAGGAAGAGT 814
              | || || || |      |||| | |||     |||||||||| || ||   |   ||||
Db       1018 GAGGTATCGACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGT 1077

Qy        815 GGTACTACCAGATAGAAATTCTGAAATTGGAAATTGGAGGCCAAAGCCTTAATCTGGACT 874
              |||| ||  || |    ||| ||    |||| ||    || ||    || ||  ||||||
Db       1078 GGTATTATGAGGTGATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACT 1137

Qy        875 GCAGAGAGTATAACGCAGACAAGGCCATCGTGGACAGTGGCACCACGCTGCTGCGCCTGC 934
              |||  ||||| |||   ||||||  ||| ||||||||||||||||    || ||  |||
Db       1138 GCAAGGAGTACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGC 1197

Qy        935 CCCAGAAGGTGTTTGATGCGGTGGTGGAAGCTGTGGCCCGCGCATCTCTGATTCCAGAAT 994
              || |||| |||||||| || |  ||  || |  |        || ||    |      | |
Db       1198 CCAAGAAAGTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGT 1257

Qy        995 TCTCTGATGGTTTCTGGACTGGGTCCCAGCTGGCGTGCTGGACGAATTCGGAAACACCTT 1054
              || |||||||||||||  ||    ||||||| |||||||              || ||||
Db       1258 TCCCTGATGGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTT 1317

Qy       1055 GGTCTTACTTCCCTAAAATCTCCATCTACCTGAGAGATGAGAACTCCAGCAGGTCATTCC 1114
              ||      |||||    |||||  ||||||| |  | ||||    ||| |  ||| ||||
Db       1318 GGAACATTTTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCC 1377

Qy       1115 GTATCACAATCCTGCCTCAGCTTTACATTCAGCCCATGATGGGGGCCGGCCTG---AATT 1171
              | ||||| ||||| || ||||  ||| | | |||  ||   |  |  | |  |    |
Db       1378 GCATCACCATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAG 1437

Qy       1172 ATGAATGTTACCGATTCGGCATTTCCCCATCCACAAATGCGCTGGTGATCGGTGCCACGG 1231
              | || ||||||   || | ||| || |  ||  | |  |      || || || ||
Db       1438 ACGACTGTTACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTA 1497

Qy       1232 TGATGGAGGGCTTCTACGTCATCTTCGACAGAGCCCAGAAGAGGGTGGGCTTCGCAGCGA 1291
              | |||||||||||||||||  |||| ||  | ||||  ||  |  | |||||  || |  |
Db       1498 TCATGGAGGGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCA 1557

Qy       1292 GCCCCTGTGCAGAAATTGCAGGTGCTGCAGTGTCTGAAATTTCCGGGCCTTTCTCAACAG 1351
              || | ||    |     |  |           | | |   |    || |||||    ||
Db       1558 GCGCTTGCCATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTCACCT 1617

Qy       1352 AGGATGTAGCCAGCAACTGTGTCCCCGCTCAGTCTTTGAGCGAGCCCATTTTGTGGATTG 1411
               |||  | |    |    |   | |  ||            |||  | |   |   ||
Db       1618 TGGACATGGAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCA 1677

Qy       1412 TGTCCTATGCGCTCATGAGCGTCTGTGGAGCCATCCTCCTTGTCTTAATCGTCCTGCTGC 1471
              |  ||||||   |      | |||| |    | || | ||     |   | || || ||
Db       1678 TAGCCTATGTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGT 1737

Qy       1472 TGCTGCCGTTCCGGTGTCAGCGTCGCCCCCGTGACCCTGAGGTCGTCAATGATGAGTCCT 1531
                | |  |  | |    |   | |  | ||   | | |||  | | |   ||||||   ||
Db       1738 GTCAGTGGCGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCT 1797

Qy       1532 CTCTGGTCA 1540
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                    | |||  | |
Db        1798 CCCTGCTGA 1806


RESULT 13
US-09-724-566A-44
; Sequence 44, Application US/09724566A
; Patent No. 6627739
; GENERAL INFORMATION:
;  APPLICANT: Anderson, John P.
;  APPLICANT:  Basi, Guriqbal
;  APPLICANT:  Doane, Minh Tam
;  APPLICANT:  Frigon, No. 6627739mand
;  APPLICANT:  John, Varghese
;  APPLICANT:  Power, Michael
;  APPLICANT:  Sinha, Sukanto
;  APPLICANT:  Tatsuno, Gwen
;  APPLICANT:  Tung, Jay
;  APPLICANT:  Wang, Shuwen
;  APPLICANT:  McConlogue, Lisa
;  TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
;  TITLE OF INVENTION:  Methods
;  FILE REFERENCE: 228-US-NEWC2
;  CURRENT APPLICATION NUMBER: US/09/724,566A
;  CURRENT FILING DATE:  2000-11-28
;  PRIOR APPLICATION NUMBER: US 09/501,708
;  PRIOR FILING DATE: 2000-02-10
;  PRIOR APPLICATION NUMBER: 60/119,571
;  PRIOR FILING DATE: 1999-02-10
;  PRIOR APPLICATION NUMBER: 60/139,172
;  PRIOR FILING DATE: 1999-06-15
;  NUMBER OF SEQ ID NOS: 104
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 44
;   LENGTH: 2348
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-724-566A-44

  Query Match             22.0%;  Score 397.4;  DB 4;  Length 2348;
  Best Local Similarity   55.0%;  Pred. No. 7.1e-85;
  Matches  863;  Conservative    0;  Mismatches  676;  Indels   30;  Gaps    3;

Qy          2 TGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCCG 61
              |||| |||   ||| |||     |    |||  |||  |||||| ||  ||   |  | |
Db        238 TGGGGGCAGGCGCCAGGGACGGACGTGGGCCAGTGCGAGCCCAGAGGGCCCGAAGGCCGG 297

Qy         62 CCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAACC 121
               ||     ||||||  || |    |  ||| |  ||  || ||| |||||    |   |
Db        298 GGCCCACCATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGC 357

Qy        122 GCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTGG 181
              |     |   ||   |  ||   | ||   ||          ||  |   |  |||
Db        358 CTGCCCACGGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCC 417

Qy        182 CGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGC---------------- 224
              | ||  |  |||  ||   ||| ||  | ||  ||  |   |||
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Db        418 CCCTGGGGCTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGG 477

Qy        225 -CAACTTCTTGGCCATGGTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGG 283
              || ||| ||| ||||| ||||||||| ||| | || || | ||||||||| |||
Db        478 GCAGCTTTGTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGG 537

Qy        284 AGATGCTGATCGGGACCCCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTA 343
              |||||    | || | |||||||||||| ||| | || || || || || || |||||||
Db        538 AGATGACCGTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTA 597

Qy        344 ACTTTGCCGTGGCAGGAACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGT 403
              ||||||| |||| |   |||| ||| ||| | |   |    ||||   | |   ||  ||
Db        598 ACTTTGCAGTGGGTGCTGCCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGT 657

Qy        404 CTAGCACATACCGCTCCAAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGA 463
              | |||||||||||   |    |    |  ||    |||   ||||| || || |  |||
Db        658 CCAGCACATACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGG 717

Qy        464 CGGGCTTCGTTGGGGAAGACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTG 523
              ||     | ||    ||||| || | ||||||| | |||  |||     || | | ||
Db        718 AAGGGGAGCTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTG 777

Qy        524 TCAACATTGCCACTATTTTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATG 583
              |||||||||  | ||   |||||||| || |||||  |    ||    || ||| | |
Db        778 CCAACATTGCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAG 837

Qy        584 GAATACTTGGCCTAGCTTATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCT 643
              | || || || || || |||||     ||||||  |||        || ||||||  | ||||
Db        838 GCATCCTGGGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCT 897

Qy        644 TCGACTCCCTGGTGACACAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAG 703
              | ||||| ||||| |  ||  |  || | |||||| | |||||| ||||| | ||||| |
Db        898 TTGACTCTCTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCAGCTTTGTGGTG 957

Qy        704 CCGGCTTGCCCGT---------TGCTGGATCTGGGACCAACGGAGGTAGTCTTGTCTTGG 754
              | ||||| ||| |          ||  |      |   | ||||||  ||  |  ||  | |
Db        958 CTGGCTTCCCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGGAGCATGATCATTG 1017

Qy        755 GTGGAATTGAACCAAGTTTGTATAAAGGAGACATCTGGTATACCCCTATTAAGGAAGAGT 814
              | ||  ||  ||  |      |||| | |||     |||||||||| ||  ||   |  ||||
Db       1018 GAGGTATCGACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGT 1077

Qy        815 GGTACTACCAGATAGAAATTCTGAAATTGGAAATTGGAGGCCAAAGCCTTAATCTGGACT 874
              ||||  ||   ||  |    |||  ||    ||||  ||    ||  ||    ||  ||  ||||||
Db       1078 GGTATTATGAGGTGATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACT 1137

Qy        875 GCAGAGAGTATAACGCAGACAAGGCCATCGTGGACAGTGGCACCACGCTGCTGCGCCTGC 934
              |||  ||||| |||   ||||||  ||| ||||||||||||||||||    ||  ||  |||
Db       1138 GCAAGGAGTACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGC 1197

Qy        935 CCCAGAAGGTGTTTGATGCGGTGGTGGAAGCTGTGGCCCGCGCATCTCTGATTCCAGAAT 994
              ||  |||| |||||||| ||  |  ||  ||  |  |        ||  ||    |      | |
Db       1198 CCAAGAAAGTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGT 1257

Qy        995 TCTCTGATGGTTTCTGGACTGGGTCCCAGCTGGCGTGCTGGACGAATTCGGAAACACCTT 1054
              ||  |||||||||||||||   ||    |||||||  |||||||              ||  ||||
Db       1258 TCCCTGATGGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTT 1317
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Qy       1055 GGTCTTACTTCCCTAAAATCTCCATCTACCTGAGAGATGAGAACTCCAGCAGGTCATTCC 1114
             ||      |||||    |||||  |||||||  |   | ||||    |||  |  |||  ||||
Db       1318 GGAACATTTTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCC 1377

Qy       1115 GTATCACAATCCTGCCTCAGCTTTACATTCAGCCCATGATGGGGGCCGGCCTG---AATT 1171
             | |||||  |||||  ||  ||||  |||  |  |  |||  ||    |   |  |  |    |
Db       1378 GCATCACCATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAG 1437

Qy       1172 ATGAATGTTACCGATTCGGCATTTCCCCATCCACAAATGCGCTGGTGATCGGTGCCACGG 1231
             | ||  ||||||    ||  |  |||  ||  |   ||   |  |   |      ||  ||  ||  ||
Db       1438 ACGACTGTTACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTA 1497

Qy       1232 TGATGGAGGGCTTCTACGTCATCTTCGACAGAGCCCAGAAGAGGGTGGGCTTCGCAGCGA 1291
             | ||||||||||||||||||  ||||  ||   |  ||||   ||   |   |  |||||  ||  |   |
Db       1498 TCATGGAGGGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCA 1557

Qy       1292 GCCCCTGTGCAGAAATTGCAGGTGCTGCAGTGTCTGAAATTTCCGGGCCTTTCTCAACAG 1351
             ||  |  ||     |      |   |              |  |  |    |     ||  |||||     ||
Db       1558 GCGCTTGCCATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTCACCT 1617

Qy       1352 AGGATGTAGCCAGCAACTGTGTCCCCGCTCAGTCTTTGAGCGAGCCCATTTTGTGGATTG 1411
              |||   |  |     |     |    |   |  ||              |||  |  |    |    ||
Db       1618 TGGACATGGAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCA 1677

Qy       1412 TGTCCTATGCGCTCATGAGCGTCTGTGGAGCCATCCTCCTTGTCTTAATCGTCCTGCTGC 1471
              |  ||||||   |       | ||||  |     | ||  |  ||      |    |  ||  ||  ||
Db       1678 TAGCCTATGTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGT 1737

Qy       1472 TGCTGCCGTTCCGGTGTCAGCGTCGCCCCCGTGACCCTGAGGTCGTCAATGATGAGTCCT 1531
               |  |   |  | |     |    |  |   |  ||    |  |  |||  |  |  |    ||||||    ||
Db       1738 GTCAGTGGCGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCT 1797

Qy       1532 CTCTGGTCA 1540
              |  |||  |  |
Db       1798 CCCTGCTGA 1806
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RESULT 14
US-09-724-566A-48
; Sequence 48, Application US/09724566A
; Patent No. 6627739
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Guriqbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, No. 6627739mand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; TITLE OF INVENTION: Methods
; FILE REFERENCE: 228-US-NEWC2

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;  CURRENT APPLICATION NUMBER: US/09/724,566A
;  CURRENT FILING DATE:  2000-11-28
;  PRIOR APPLICATION NUMBER: US 09/501,708
;  PRIOR FILING DATE: 2000-02-10
;  PRIOR APPLICATION NUMBER: 60/119,571
;  PRIOR FILING DATE: 1999-02-10
;  PRIOR APPLICATION NUMBER: 60/139,172
;  PRIOR FILING DATE: 1999-06-15
;  NUMBER OF SEQ ID NOS: 104
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 48
;   LENGTH: 16080
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Expression Vector pCEK
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(16080)
;   OTHER INFORMATION: n = A,T,C or G
US-09-724-566A-48

  Query Match             22.0%;  Score 397.4;  DB 4;  Length 16080;
  Best Local Similarity   55.0%;  Pred. No. 1.5e-84;
  Matches  863;  Conservative    0;  Mismatches  676;  Indels   30;  Gaps    3;

Qy          2 TGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCCG 61
              |||| |||   ||| |||     |    |||  |||  |||||| ||  ||   |  | |
Db       1607 TGGGGGCAGGCGCCAGGGACGGACGTGGGCCAGTGCGAGCCCAGAGGGCCCGAAGGCCGG 1666

Qy         62 CCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAACC 121
               ||     ||||||  || |    |  ||| |  ||  || ||| |||||    |   |
Db       1667 GGCCCACCATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGC 1726

Qy        122 GCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTGG 181
               |     |   ||   |  ||   | ||   ||         ||  |   |  |||
Db       1727 CTGCCCACGGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCC 1786

Qy        182 CGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGC---------------- 224
              | || |  |||  ||   ||| || | ||  ||  |   |||
Db       1787 CCCTGGGGCTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGG 1846

Qy        225 -CAACTTCTTGGCCATGGTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGG 283
               || |||  |||  ||||| |||||||||  |||  | || || |  |||||||| |||
Db       1847 GCAGCTTTGTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGG 1906

Qy        284 AGATGCTGATCGGGACCCCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTA 343
              |||||    | || | |||||||||||| |||  | || || || || || || |||||||
Db       1907 AGATGACCGTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTA 1966

Qy        344 ACTTTGCCGTGGCAGGAACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGT 403
              ||||||| ||||  |   |||| ||| ||| | |  |    ||||  | |  ||  ||
Db       1967 ACTTTGCAGTGGGTGCTGCCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGT 2026

Qy        404 CTAGCACATACCGCTCCAAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGA 463
              | |||||||||||  |    |    |  ||    |||   ||||| || || |  |||
Db       2027 CCAGCACATACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGG 2086
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```
Qy        464 CGGGCTTCGTTGGGGAAGACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTG 523
Db       2087 AAGGGGAGCTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTG 2146

Qy        524 TCAACATTGCCACTATTTTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATG 583
Db       2147 CCAACATTGCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAG 2206

Qy        584 GAATACTTGGCCTAGCTTATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCT 643
Db       2207 GCATCCTGGGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCT 2266

Qy        644 TCGACTCCCTGGTGACACAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAG 703
Db       2267 TTGACTCTCTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCAGCTTTGTGGTG 2326

Qy        704 CCGGCTTGCCCGT----------TGCTGGATCTGGGACCAACGGAGGTAGTCTTGTCTTGG 754
Db       2327 CTGGCTTCCCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGGAGCATGATCATTG 2386

Qy        755 GTGGAATTGAACCAAGTTTGTATAAAGGAGACATCTGGTATACCCCTATTAAGGAAGAGT 814
Db       2387 GAGGTATCGACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGT 2446

Qy        815 GGTACTACCAGATAGAAATTCTGAAATTGGAAATTGGAGGCCAAAGCCTTAATCTGGACT 874
Db       2447 GGTATTATGAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACT 2506

Qy        875 GCAGAGAGTATAACGCAGACAAGGCCATCGTGGACAGTGGCACCACGCTGCTGCGCCTGC 934
Db       2507 GCAAGGAGTACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGC 2566

Qy        935 CCCAGAAGGTGTTTGATGCGGTGGTGGAAGCTGTGGCCCGCGCATCTCTGATTCCAGAAT 994
Db       2567 CCAAGAAAGTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGT 2626

Qy        995 TCTCTGATGGTTTCTGGACTGGGTCCCAGCTGGCGTGCTGGACGAATTCGGAAACACCTT 1054
Db       2627 TCCCTGATGGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTT 2686

Qy       1055 GGTCTTACTTCCCTAAAATCTCCATCTACCTGAGAGATGAGAACTCCAGCAGGTCATTCC 1114
Db       2687 GGAACATTTTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCC 2746

Qy       1115 GTATCACAATCCTGCCTCAGCTTTACATTCAGCCCATGATGGGGGCCGGCCTG---AATT 1171
Db       2747 GCATCACCATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAG 2806

Qy       1172 ATGAATGTTACCGATTCGGCATTTCCCCATCCACAAATGCGCTGGTGATCGGTGCCACGG 1231
Db       2807 ACGACTGTTACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTA 2866

Qy       1232 TGATGGAGGGCTTCTACGTCATCTTCGACAGAGCCCAGAAGAGGGTGGGCTTCGCAGCGA 1291
Db       2867 TCATGGAGGGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCA 2926
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```
Qy       1292 GCCCCTGTGCAGAAATTGCAGGTGCTGCAGTGTCTGAAATTTCCGGGCCTTTCTCAACAG 1351
             ||  |  ||    |     |   |           | | |   |    ||  |||||    ||
Db       2927 GCGCTTGCCATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTCACCT 2986

Qy       1352 AGGATGTAGCCAGCAACTGTGTCCCCGCTCAGTCTTTGAGCGAGCCCATTTTGTGGATTG 1411
              |||  | |    |     |   |  |  ||            |||  | |   |   ||
Db       2987 TGGACATGGAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCA 3046

Qy       1412 TGTCCTATGCGCTCATGAGCGTCTGTGGAGCCATCCTCCTTGTCTTAATCGTCCTGCTGC 1471
             |  ||||||   |      | ||||  |    | ||  | ||     |   | ||  ||  ||
Db       3047 TAGCCTATGTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGT 3106

Qy       1472 TGCTGCCGTTCCGGTGTCAGCGTCGCCCCCGTGACCCTGAGGTCGTCAATGATGAGTCCT 1531
               | |  |  | |    |   | |  | ||   | | ||| | | |   ||||||   ||
Db       3107 GTCAGTGGCGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCT 3166

Qy       1532 CTCTGGTCA 1540
              | ||| | |
Db       3167 CCCTGCTGA 3175
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RESULT 15
US-09-724-566A-1
; Sequence 1, Application US/09724566A
; Patent No. 6627739
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Guriqbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, No. 6627739mand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; TITLE OF INVENTION: Methods
; FILE REFERENCE: 228-US-NEWC2
; CURRENT APPLICATION NUMBER: US/09/724,566A
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1503
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-566A-1

Query Match 21.9%; Score 395; DB 4; Length 1503;

Best Local Similarity 55.6%; Pred. No. 2.2e-84;
Matches 805; Conservative 0; Mismatches 630; Indels 12; Gaps 2;

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Qy      106 GCCGCGGCCACGAACCGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGC 165
            |||   | |||  | | ||   |   ||   ||| | |   |||       | ||  | |
Db       55 GCCCACGGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCC 114

Qy      166 CACGCCGACGGCTTGGCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCC 225
            |  |       |  || | |  |     ||    |  |  | |   ||||   |    | |
Db      115 CTGGGGCTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGC 174

Qy      226 AACTTCTTGGCCATGGTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAG 285
            | |||  |||  ||||| |||||||||  |||  | || || |  |||||||| |||||
Db      175 AGCTTTGTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAG 234

Qy      286 ATGCTGATCGGGACCCCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAAC 345
            |||    | || | |||||||||| |||  | || || || || || || |||||||||
Db      235 ATGACCGTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAAC 294

Qy      346 TTTGCCGTGGCAGGAACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCT 405
            |||||  ||||  |   |||| ||| ||| | |   |    ||||   | |   ||  |||
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Job time : 161 secs

GenCore version 5.1.6

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Searched: 2421054 seqs, 1828716029 residues

Total number of hits satisfying chosen parameters: 4842108

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

RESULT 1
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; Sequence 1, Application US/09794927
; Patent No. US20010016324A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.

; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,
AND
; TITLE OF INVENTION: USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280FG
; CURRENT APPLICATION NUMBER: US/09/794,927
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
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;   LENGTH: 1804
;   TYPE: DNA
;   ORGANISM: Homo sapiens
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; Sequence 1, Application US/09795847
; Patent No. US20010018208A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES

; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280DE
; CURRENT APPLICATION NUMBER: US/09/795,847
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1804
; TYPE: DNA
; ORGANISM: Homo sapiens

US-09-795-847-1

Query Match 100.0%; Score 1804; DB 9; Length 1804;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1804; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60
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Db          1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60

Qy         61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120
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Db         61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120

Qy        121 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180
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Qy        181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240
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Qy        241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300
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Db        241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300

Qy        301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360
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Db        361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420

Qy        421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480
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Db        421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480
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Qy        481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540
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Db        481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540

Qy        541 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600
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Db        541 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600

Qy        601 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 660
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Db        601 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 660

Qy        661 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 720
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Db        661 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 720

Qy        721 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 780
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Db        721 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 780

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Qy        901 ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG 960
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Qy       1381 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1440
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Db       1381 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1440

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Qy       1501 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1560
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Qy       1561 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1620
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Db       1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1680

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Qy       1801 AAAA 1804
             ||||
Db       1801 AAAA 1804
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RESULT 3
US-09-794-743-1
; Sequence 1, Application US/09794743
; Patent No. US20010021391A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280BC
; CURRENT APPLICATION NUMBER: US/09/794,743
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493

; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1804
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-794-743-1

Query Match 100.0%; Score 1804; DB 9; Length 1804;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1804; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60
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Qy        181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240
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Qy        421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480
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Db        421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480

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Db        481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540

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Db        541 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600

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Db        601 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 660

Qy        661 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 720
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Db        661 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 720

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Db        781 GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA 840

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Qy       1141 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA 1200
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Qy       1261 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1320
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Db       1321 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1380

Qy       1381 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1440
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Qy       1801 AAAA 1804
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Db       1801 AAAA 1804
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RESULT 4
US-09-794-748-1
; Sequence 1, Application US/09794748
; Patent No. US20020037315A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280JL
; CURRENT APPLICATION NUMBER: US/09/794,748
; CURRENT FILING DATE: 2001-02-27
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; PRIOR APPLICATION NUMBER: PCT/US99/20881
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; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24

; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 1804
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-794-748-1

  Query Match 100.0%; Score 1804; DB 9; Length 1804;
  Best Local Similarity 100.0%; Pred. No. 0;
  Matches 1804; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60
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Qy         61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120
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Qy        121 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180
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Db        181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240

Qy        241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300

Qy        301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360

Qy        361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420

Qy        421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480
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Db        421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480

Qy        481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540

Qy        541 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600
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Db        541 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600

Qy        601 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 660
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Db        601 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 660

Qy        661 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 720
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Db        661 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 720

Qy        721 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 780

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Qy        781 GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA 840

Db        781 GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA 840

Qy        841 TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC 900

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Qy        901 ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG 960

Db        901 ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG 960

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Db       1021 CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC 1080

Qy       1081 TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1140

Db       1081 TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1140

Qy       1141 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA 1200

Db       1141 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA 1200

Qy       1201 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC 1260

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Db       1321 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1380

Qy       1381 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1440

Db       1381 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1440

Qy       1441 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1500

Db       1441 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1500

Qy       1501 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1560
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Db        1501 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1560

Qy        1561 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1620
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1561 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1620

Qy        1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1680
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1680

Qy        1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740
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Db        1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740

Qy        1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAAACCAAAAAAAAAAA 1800
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Db        1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAAACCAAAAAAAAAAA 1800

Qy        1801 AAAA 1804
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Db        1801 AAAA 1804
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RESULT 5
US-09-794-925-1
; Sequence 1, Application US/09794925
; Patent No. US20020064819A1
; GENERAL INFORMATION:
;  APPLICANT:  Gurney, Mark E.
;  APPLICANT:  Bienkowski, Michael J.
;  APPLICANT:  Heinrikson, Robert L.
;  APPLICANT:  Parodi, Luis A.
;  APPLICANT:  Yan, Riqiang
;  TITLE OF INVENTION:  ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,
AND USES
;  TITLE OF INVENTION:  THEREFOR
;  FILE REFERENCE:  28341/6280HI
;  CURRENT APPLICATION NUMBER: US/09/794,925
;  CURRENT FILING DATE:  2001-02-27
;  PRIOR APPLICATION NUMBER:  09/416,901
;  PRIOR FILING DATE:  1999-10-13
;  PRIOR APPLICATION NUMBER:  60/155,493
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  09/404,133
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  PCT/US99/20881
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  60/101,594
;  PRIOR FILING DATE:  1998-09-24
;  NUMBER OF SEQ ID NOS:  73
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 1804
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-794-925-1
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Query Match 100.0%; Score 1804; DB 9; Length 1804;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1804; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60

Qy         61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120
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Db         61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120

Qy        121 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180
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Db        121 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180

Qy        181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240
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Db        181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240

Qy        241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300
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Db        241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300

Qy        301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360
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Db        301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360

Qy        361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420
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Db        361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420

Qy        421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480
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Db        421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480

Qy        481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540

Qy        541 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600
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Db        541 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600

Qy        601 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 660
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Db        601 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 660

Qy        661 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 720
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Db        661 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 720

Qy        721 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 780
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Db        721 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 780

Qy        781 GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA 840
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Db        781 GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA 840

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Db        841 TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC 900

Qy        901 ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG 960
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Db        901 ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG 960

Qy        961 GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC 1020
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Db        961 GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC 1020

Qy       1021 CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC 1080
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Qy       1081 TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1140
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Db       1141 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA 1200

Qy       1201 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC 1260
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Db       1201 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC 1260

Qy       1261 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1320
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Db       1261 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1320

Qy       1321 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1380

Qy       1381 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1440

Qy       1441 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1500

Qy       1501 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1560

Qy       1561 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1620

Qy       1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1680
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Db        1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1680

Qy        1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740
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Db        1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740

Qy        1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAAACCAAAAAAAAAAA 1800
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Db        1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAAACCAAAAAAAAAAA 1800

Qy        1801 AAAA 1804
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Db        1801 AAAA 1804
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RESULT 6
US-09-681-442-1
; Sequence 1, Application US/09681442
; Patent No. US20020081634A1
; GENERAL INFORMATION:
;  APPLICANT: Gurney, Mark E.
;  APPLICANT:  Bienkowski, Michael J.
;  APPLICANT:  Heinrikson, Robert L.
;  APPLICANT:  Parodi, Luis A.
;  APPLICANT:  Yan, Riqiang
;  TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,
AND USES
;  TITLE OF INVENTION:  THEREFOR
;  FILE REFERENCE: 28341/6280FG
;  CURRENT APPLICATION NUMBER: US/09/681,442
;  CURRENT FILING DATE:  2001-04-05
;  PRIOR APPLICATION NUMBER: 09/416,901
;  PRIOR FILING DATE: 1999-10-13
;  PRIOR APPLICATION NUMBER: 60/155,493
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 1804
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-681-442-1

  Query Match           100.0%;  Score 1804;  DB 9;  Length 1804;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1804;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60
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Db          1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60
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Qy        61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120
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Db        61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120

Qy       121 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       121 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180

Qy       181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240

Qy       241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300
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Qy       301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360
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Db       301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360

Qy       361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420
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Db       361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420

Qy       421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480
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Db       421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480

Qy       481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540
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Db       481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540

Qy       541 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       541 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600

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Db       601 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 660

Qy       661 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 720
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Db       661 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 720

Qy       721 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 780
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Db       721 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 780

Qy       781 GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA 840
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Db       781 GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA 840

Qy       841 TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC 900
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Db       841 TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC 900

Qy       901 ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG 960
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Qy        961 GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC 1020
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC 1020

Qy       1021 CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC 1080
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC 1080

Qy       1081 TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1140
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1140

Qy       1141 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA 1200
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA 1200

Qy       1201 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC 1260
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC 1260

Qy       1261 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1320
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1320

Qy       1321 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1380
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1380

Qy       1381 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1440
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1440

Qy       1441 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1500
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1500

Qy       1501 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1560
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1560

Qy       1561 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1620
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1620

Qy       1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1680
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1680

Qy       1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740

Qy       1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAAACCAAAAAAAAAAA 1800
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAAACCAAAAAAAAAAA 1800

Qy        1801 AAAA 1804
               ||||
Db        1801 AAAA 1804
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RESULT 7
US-09-869-414-1
; Sequence 1, Application US/09869414
; Publication No. US20030077226A1
; GENERAL INFORMATION:
;  APPLICANT: Beinkowski et al.
;  TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,
AND USES
;  TITLE OF INVENTION:  THEREFOR
;  FILE REFERENCE: 28341/6280M
;  CURRENT APPLICATION NUMBER: US/09/869,414
;  CURRENT FILING DATE:  2001-06-27
;  PRIOR APPLICATION NUMBER: 09/416,901
;  PRIOR FILING DATE: 1999-10-13
;  PRIOR APPLICATION NUMBER: 60/155,493
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 1804
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-869-414-1

  Query Match             100.0%;  Score 1804;  DB 10;  Length 1804;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1804;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60

Qy         61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120

Qy        121 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180

Qy        181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240
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Qy        241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300

Qy        301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360

Qy        361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420

Qy        421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480

Qy        481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540

Qy        541 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600

Qy        601 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 660

Qy        661 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 720

Qy        721 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 780

Qy        781 GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA 840

Qy        841 TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC 900

Qy        901 ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG 960

Qy        961 GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC 1020

Qy       1021 CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC 1080

Qy       1081 TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1140
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                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1081 TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1140

Qy        1141 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA 1200
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1141 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA 1200

Qy        1201 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC 1260
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1201 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC 1260

Qy        1261 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1320
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1261 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1320

Qy        1321 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1380
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1321 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1380

Qy        1381 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1440
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1381 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1440

Qy        1441 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1500
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1441 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1500

Qy        1501 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1560
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1501 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1560

Qy        1561 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1620
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1561 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1620

Qy        1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1680
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1680

Qy        1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740

Qy        1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAAACCAAAAAAAAAAA 1800
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAAACCAAAAAAAAAAA 1800

Qy        1801 AAAA 1804
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Db        1801 AAAA 1804
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RESULT 8
US-09-548-366-1
; Sequence 1, Application US/09548366
; Publication No. US20030104365A1
; GENERAL INFORMATION:

; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES THEREFOR
; FILE REFERENCE: 28341/6280A
; CURRENT APPLICATION NUMBER: US/09/548,366
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1804
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-548-366-1

  Query Match 100.0%; Score 1804; DB 10; Length 1804;
  Best Local Similarity 100.0%; Pred. No. 0;
  Matches 1804; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60

Qy         61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120

Qy        121 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180

Qy        181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240

Qy        241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300

Qy        301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360

Qy        361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420

Qy        421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480

Qy        481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540

Qy        541 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600

Qy        601 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 660

Qy        661 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 720

Qy        721 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 780

Qy        781 GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA 840

Qy        841 TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC 900

Qy        901 ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG 960

Qy        961 GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC 1020

Qy       1021 CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC 1080

Qy       1081 TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1140

Qy       1141 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA 1200

Qy       1201 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC 1260
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Qy       1261 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1320

Qy       1321 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1380

Qy       1381 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1440
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Qy       1801 AAAA 1804
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RESULT 9
US-09-978-295A-195
; Sequence 195, Application US/09978295A
; Patent No. US20020156006A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C11
; CURRENT APPLICATION NUMBER: US/09/978,295A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
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; PRIOR APPLICATION NUMBER: 60/065311
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 98.9%; Score 1784.4; DB 9; Length 1879;
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RESULT 10
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; Sequence 195, Application US/09978697
; Patent No. US20020169284A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
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; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C27
; CURRENT APPLICATION NUMBER: US/09/978,697
; CURRENT FILING DATE: 2001-10-16
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; PRIOR APPLICATION NUMBER: 60/085697

Query Match 98.9%; Score 1784.4; DB 9; Length 1879;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1785; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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; Patent No. US20020177553A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C9
; CURRENT APPLICATION NUMBER: US/09/978,192A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 98.9%; Score 1784.4; DB 9; Length 1879;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1785; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60
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Qy        301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360
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Db        394 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 453

Qy        361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420
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Db        454 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 513

Qy        421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480
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Db        514 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 573

Qy        481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540
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Db        574 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 633

Qy        541 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600
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Db        634 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 693

Qy        601 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 660
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Db        694 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 753

Qy        661 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 720
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Db        754 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 813

Qy        721 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 780
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Db        814 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 873

Qy        781 GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA 840
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Db        874 GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA 933

Qy        841 TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC 900
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Db        934 TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC 993

Qy        901 ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG 960
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Qy        961 GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC 1020
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Db       1054 GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC 1113

Qy       1021 CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC 1080
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Db       1114 CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC 1173

Qy       1081 TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1140
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Db       1174 TACCTGAGAGACGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1233

Qy       1141 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA 1200
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Db       1294 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC 1353

Qy       1261 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1320
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Db       1354 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1413

Qy       1321 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1380
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Db       1414 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1473

Qy       1381 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1440
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Db       1474 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1533

Qy       1441 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1500
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Db       1534 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1593

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Db       1594 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1653

Qy       1561 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1620
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Db       1654 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1713

Qy       1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1680
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Qy       1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740
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RESULT 12
US-09-999-832A-195
; Sequence 195, Application US/09999832A
; Publication No. US20020192706A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C63
; CURRENT APPLICATION NUMBER: US/09/999,832A
; CURRENT FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
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; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 98.9%; Score 1784.4; DB 9; Length 1879;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1785; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db        154 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 213

Qy        121 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180
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Db       1174 TACCTGAGAGACGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1233

Qy       1141 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA 1200
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Db        1234 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA 1293

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Qy        1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1680
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Db        1834 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAA 1879
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RESULT 13
US-09-978-189-195
; Sequence 195, Application US/09978189
; Publication No. US20030004102A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C7
; CURRENT APPLICATION NUMBER: US/09/978,189
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
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; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
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; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077641
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; PRIOR APPLICATION NUMBER: 60/077791
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; PRIOR APPLICATION NUMBER: 60/078886
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078936
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078939
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26

; PRIOR APPLICATION NUMBER: 60/079664
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079663
; PRIOR FILING DATE: 1998-03-27
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; PRIOR APPLICATION NUMBER: 60/080328
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 98.9%; Score 1784.4; DB 10; Length 1879;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1785; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60
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Db         94 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 153

Qy         61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120
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Db        154 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 213

Qy        121 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180
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Db        214 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 273

Qy        181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        274 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 333

Qy        241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        334 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 393

Qy        301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360
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Db        394 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 453

Qy        361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420
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Db        454 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 513

Qy        421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480
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Db        514 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 573

Qy        481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540
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Db        574 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 633
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Qy        541 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        634 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 693

Qy        601 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 660
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Db        694 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 753

Qy        661 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        754 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 813

Qy        721 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 780
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Db        814 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 873

Qy        781 GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        874 GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA 933
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Qy        841 TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        934 TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC 993

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Db        994 ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG 1053

Qy        961 GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC 1020
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Db       1054 GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC 1113

Qy       1021 CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC 1080
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Db       1114 CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC 1173

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Db       1174 TACCTGAGAGACGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1233

Qy       1141 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA 1200
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Db       1294 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC 1353

Qy       1261 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1320
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Db       1354 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1413

Qy       1321 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1380
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Db       1474 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1533

Qy       1441 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1500
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Db       1534 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1593

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Qy       1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1680
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Db       1834 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAA 1879
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RESULT 14
US-09-978-608A-195
; Sequence 195, Application US/09978608A
; Publication No. US20030045462A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
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; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
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; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.

; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C22
; CURRENT APPLICATION NUMBER: US/09/978,608A
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 195
; LENGTH: 1879
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-978-608A-195

Query Match 98.9%; Score 1784.4; DB 10; Length 1879;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1785; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db         94 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 153

Qy         61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        154 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 213

Qy        121 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180
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Db        214 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 273

Qy        181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        274 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 333

Qy        241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300
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Db        334 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 393

Qy        301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360
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Db        394 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 453

Qy        361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        454 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 513

Qy        421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        514 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 573

Qy        481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        574 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 633
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Qy       541 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600
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Db       634 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 693

Qy       601 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       694 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 753

Qy       661 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       754 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 813

Qy       721 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       814 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 873

Qy       781 GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA 840
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Db       874 GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA 933
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Qy       841 TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC 900
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Db       934 TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC 993

Qy       901 ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG 960
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       994 ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG 1053

Qy       961 GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC 1020
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1054 GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC 1113

Qy      1021 CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC 1080
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1114 CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC 1173

Qy      1081 TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1140
            |||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db      1174 TACCTGAGAGACGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1233

Qy      1141 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA 1200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1234 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA 1293

Qy      1201 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC 1260
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1294 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC 1353

Qy      1261 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1320
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1354 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1413

Qy      1321 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1380
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1414 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1473

Qy      1381 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1440
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1474  CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1533

Qy        1441  GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1500
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1534  GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1593

Qy        1501  CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1560
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1594  CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1653

Qy        1561  GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1620
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1654  GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1713

Qy        1621  AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1680
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1714  AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1773

Qy        1681  GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740
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Qy        1741  CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAA 1786
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RESULT 15
US-09-978-585A-195
; Sequence 195, Application US/09978585A
; Publication No. US20030049633A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C15
; CURRENT APPLICATION NUMBER: US/09/978,585A
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 195
;   LENGTH: 1879
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-978-585A-195

Query Match 98.9%; Score 1784.4; DB 10; Length 1879;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1785; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60
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Db      94 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 153

Qy      61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     154 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 213

Qy     121 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     214 CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 273

Qy     181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     274 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 333

Qy     241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     334 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 393

Qy     301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360
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Db     394 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 453

Qy     361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy     421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     514 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 573

Qy     481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     574 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 633

Qy     541 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600
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Db        634 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 693

Qy        601 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 660

Db        694 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 753

Qy        661 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 720

Db        754 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 813

Qy        721 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 780

Db        814 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 873

Qy        781 GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA 840

Db        874 GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA 933

Qy        841 TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC 900

Db        934 TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC 993

Qy        901 ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG 960

Db        994 ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG 1053

Qy        961 GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC 1020

Db       1054 GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC 1113

Qy       1021 CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC 1080

Db       1114 CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC 1173

Qy       1081 TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1140

Db       1174 TACCTGAGAGACGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC 1233

Qy       1141 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA 1200

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Qy       1201 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC 1260

Db       1294 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC 1353

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Qy       1321 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1380

Db       1414 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1473

Qy       1381 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1440
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Db        1474 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1533

Qy        1441 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1500
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1534 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1593

Qy        1501 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1560
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1594 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1653

Qy        1561 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1620
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1654 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1713

Qy        1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1680
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1714 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1773

Qy        1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1774 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1833

Qy        1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAA 1786
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Job time : 662 secs